IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Ruben et al..

Application Serial No.: 09/880,748 | Group Art Unit: 1631

Filed: June 15, 2001 | Examiner: DUFFY, Patricia

Title: ANTIBODIES THAT IMMUNOSPECIFICALLY BIND TO B LYMPHOCYTE STIMULATOR PROTEIN (as amended)

Atty. Docket No. PF523P1

DECLARATION OF RODGER SMITH UNDER 37 C.F.R. § 1.132

Commissioner for Patents
Alexandria, VA 22313-1450

Sir:

I, Rodger Smith Ph.D., hereby declare and state as follows:

1. I am currently employed as a Senior Scientist I in the Lead Product Development group at Human Genome Sciences, Inc. (HGS), which I understand to be the assignee of the above-captioned patent application. I earned my Ph.D. in 1989 from the Department of Microbiology at the University of Illinois, Urbana -Champaign, Illinois. It was during my thesis research that I first began work on cloning and sequencing of antibody genes. From 1990 to 1999, I worked as a Scientist in the Molecular Biology and Assay Development groups at IGEN International, Inc. (now known as Bioveris Corp.) where my primary responsibilities were developing and characterizing antibody reagents for therapeutic and diagnostic applications. A portion of this work entailed the design and construction of both human and mouse V-domain antibody repertoire libraries for display on the surface of bacteriophage including in 1997 an SBIR grant sponsored by The Department of the Army to construct and validate a large semi-synthetic human phage antibody display library. In 2000, I joined the Antibody Development group (now known as the Lead Product Development group) at Human Genome Sciences where I have

continued to work with phage antibody display technology, primarily for developing therapeutic antibodies to a variety of novel protein targets. A large portion of this work involved screening and characterizing hundreds of antibody leads at both the DNA sequence and protein level. I am the co-author of 12 scientific articles and several issued and pending patent applications. A copy of my curriculum vitae is attached as Exhibit A.

2. I have been shown and have examined U.S. Patent Application No. 09/880,748 (the '748 Application), captioned above, which I understand was filed on June 15, 2001. I will refer to the '748 Application as "the Application."

3. I have been shown and have examined Table 1 and the Sequence Listing of U.S. Patent Application No. U.S. Patent Application No. 60/212,210 (the '210 Application), which I understand was filed on June 16, 2000. It is my understanding that Table 1 and SEQ ID NOS 1-2128 of the Sequence Listing of the '748 and the '210 applications are identical.

4. I have been asked by patent counsel for Human Genome Sciences to explain how an antibody scientist familiar with the sequences of antibodies would be able to accurately recognize the beginning of an immunoglobulin light chain variable domain (VL domain) in the amino acid sequence of an scFv protein. Moreover, I have been asked if and how an antibody scientist, based on the information presented in Table 1 of the '748 application and the sequences shown in SEQ ID NOS:1-2128 would have been able to identify and correct any errors in the delineation of the VL domain in column 3 of Table 1.

BACKGROUND

5. Intact immunoglobulin (i.e., antibody) molecules are composed of heavy chain polypeptides and light chain polypeptides that are joined together by disulfide bonds. Each heavy and light chain can be further subdivided into a Variable (V) and a Constant (C) region. The variable regions of the heavy and light chains of a given antibody make up the antigen binding-portion an antibody. The variable regions of heavy chains are known as VH domains and the variable regions of light chains are known as VL domains. The constant region of an immunoglobulin heavy chain determines the effector functions of an antibody (e.g. the ability to activate complement or the ability to cross the placenta).

The constant regions of light chains serve more of a structural role, allowing the light chain to associate with the heavy chain by disulfide bonding. Constant regions are further subdivided into particular isotypes, based on the sequences of these regions. There are five classes of heavy chain isotypes known as IgA, IgG, IgM, IgD, and IgE and two classes of light chain isotypes known as kappa and lambda.

6. For the purposes of this Declaration it is necessary to understand that there are distinct sets of immunoglobulin variable regions that are found in association with kappa constant regions and lambda constant regions, respectively. These two sets of variable regions are encoded by two different loci in the human genome. The variable regions that associate with kappa constant regions are referred to as Vκ (for Variable kappa) while the variable regions that associate with lambda constant regions are referred to Vλ (for Variable lambda).

7. It is also useful to understand that the sequences of the variable regions of both heavy and light chain genes encoded by the genome are referred to as "germline" sequences. The sequences encoding the variable regions of an antibody may be mutated in the course of the life of an antibody-producing B cell through a process called somatic hypermutation. The variable regions of an antibody obtained from a B cell that has undergone somatic hypermutation will have sequences that deviate from the precise sequence of the germline sequence.

8. An scFv is a single chain antibody that is (usually) produced using phage display technology in which the amino acid sequence of an immunoglobulin heavy chain variable domain (VH domain) is linked to the amino acid sequence of an immunoglobulin light chain variable domain (VL domain) by a synthetic linker sequence. The resulting scFv protein is conformationally similar to the antigen binding region of an intact antibody. ScFvs may contain VH and VL regions that have germline or non-germline sequences.

DEFINING THE SEQUENCE OF THE VL REGION IN AN SCFV

9. The beginning of the VL region in an scFv may be easily delineated by 1) determining whether the scFv contains a kappa or a lambda variable domain and then 2)

calculating the first amino acid sequence based on a standard numbering system for immunoglobulin variable regions that was established by Elvin A. Kabat and Tai Te Wu in the 1970's that is widely used by immunologists even today. This is explained in more detail below.

Determining if the VL in the scFv is a Vκ or a Vλ

10. It is clear from the specification of the '748 Application that the scFvs described in Table 1 and shown in the sequence listing contain human VH and VL regions. Paragraph [0298] indicates the scFvs are "human scFvs" and that each scFv sequence in the Sequence Listing is annotated as being from "Homo sapiens." It is also clear from the specification of the '748 Application that the scFvs described in Table 1 and shown in the sequence listing contain a linker region that contains a core sequence of 15 amino acid residues consisting of Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser (or $(Gly_4Ser)_3$). As an example, take the scFv of SEQ ID NO:1 which is described in Table 1 at page 287 to comprise the amino acid sequence of a VH domain consisting of amino acids 1 - 122 of SEQ ID NO:1 and an amino acid sequence of a VL domain consisting of amino acids 138 – 248 of SEQ ID NO:1. Therefore, the linker sequence in-between (i.e., of amino acids 123-137 of SEQ ID NO:1) consists of the sequence $(Gly_4Ser)_3$. Inspection of each of the scFvs reveals that the linker sequence of amino acids between the end of the VH and the start of the VL as defined in Table 1 contains the $(Gly_4Ser)_3$ sequence.

11. Before June 16, 2000 the sequences of most, if not all human Vκ and Vλ were known. Attached hereto as Exhibits B-D are printouts from a database of immunoglobulin genes called IgBLAST maintained by the National Center for Biotechnology (NCBI). This database may be accessed on the world wide web at http://www.ncbi.nlm.nih.gov/igblast/showGermline.cgi. Exhibit B briefly explains the composition of the sequences in the subset of the IgBLAST database that contains the sequences of germline genes. At the bottom of Exhibit B one can see a series of pull down menus that enable a user to see a set of known of sequences (either amino acid or polynucleotide sequences) for germline genes from a given organism for several loci, including Vκ and Vλ loci.

12. Exhibits C and D, respectively, show the contents of the germline database when a user requests to see the protein sequences of either human Vκ or human Vλ germline genes. At the top of page one of both Exhibits C and D it is clear that the sequences on the germline genes were taken from scientific work that was performed and published prior to June 16, 2000.

13. Thus, as described in the '748 application, at paragraph [0669], it would be routine to align the sequences of each the 2128 scFvs disclosed in Table 1, against known human germline VL (both Vκ and Vλ) sequences to determine if a given scFv contains a kappa or a lambda variable region. This would be accomplished by identifying whether the "closest germline" VL domain is a Vκ or a Vλ. The results of aligning the scFvs of each of SEQ ID NOS:1-2128 against a database containing the sequences of the 36 human Vλ and 46 human Vκ genes identified in NCBI's human IgBLAST database are shown in a table attached hereto as Exhibit E. The first column of the table in Exhibit E indicates the SEQ ID NO of the scFv, the second column indicates the name of germline gene that is most similar to the VL region of the scFv, the third column indicates the isotype (kappa or lambda) of the germline gene shown in column 2 and the fourth column indicates the percent identity between the VL region of the scFv and the closest germline gene.

Kabat-Wu Numbering System

14. Elvin A. Kabat and Tai Te Wu developed a numbering system for consistent amino acid numbering of immunoglobulin variable regions that would result in certain amino acid numbers always being assigned to CDR regions of VH, Vκ or Vλ regions. With respect to light chain variable regions, Kabat and Wu, through extensive analysis of many light chain variable regions recognized that there is an invariant cysteine residue at what they define as position 23 of an immunoglobulin light chain variable. This statement is supported by a sentence in the abstract of Johnson and Wu[1] (provided herewith as Exhibit F) which indicates the CDR1 of light chains begins after the first invariant cysteine at position no. 23 in light chains. Moreover, at the top of the right hand column on page 214, Johnson and Wu indicate that the Kabat-Wu numbering scheme is more clearly set forth in the Introduction of the fifth edition of a book Kabat, Wu and

others complied entitled *Sequences of Proteins of Immunological Interest*[2], a portion of which is attached hereto as Exhibit G. Table 1 from the Introduction of *Sequences of Proteins of Immunological Interest* explains that the sequence of amino acids prior to the first CDR region light chains is numbered from 1-23 (of which amino acid 23 is the invariant cysteine), but that lambda chains contain a deletion (i.e., have no amino acid corresponding to) what Kabat-Wu number as amino acid position 10 in light chains. In effect, this makes the invariant cysteine residue in lambda light chains occur at the 22nd amino acid residue in lambda light chains. This invariant cysteine at the 22nd amino acid residue of lambda light chains and the 23rd amino acid residue of kappa light chains (both of which are referred to as the invariant cysteine residue at position no. 23 by the Kabat-Wu numbering scheme), can be used to accurately identify the first amino acid residue in the VL region of an scFv light chain, after one has identified whether the VL region is a Vκ or Vλ as described above.

15. Thus, to identify the first amino acid position of the VL region, one simply must identify the cysteine amino acid residue that is approximately 23 amino acid residues after the $(Gly_4Ser)_3$ sequence in the linker region. Having identified this cysteine residue, then one assigns it as amino acid residue number 23 or 22, depending on whether the closest identified germline gene is a kappa or lambda variable region, respectively. Finally one must simply count backwards to 1 to identify the first amino acid of the VL region.

16. As a general rule, the first cysteine residue after the $(Gly_4Ser)_3$ sequence in the linker region will be the cysteine residue that Kabat-Wu defines as the cysteine at amino acid position No. 23. In the 2128 scFv sequences disclosed in Table 1 and the Sequence Listing of the '748 application, there are only 4 cases where the first cysteine residue after the $(Gly_4Ser)_3$ sequence in the linker region is not the cysteine residue defined by Kabat-Wu numbering as position number 23. The exceptions include:

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[1] Johnson, G. and T. T. Wu. (2000) Kabat Database and its application: 30 years after the first variability plot.. Nucleic Acids research 28:214-218
[2] Kabat E.A., et al. (1991) *Sequences of Proteins of Immunological Interest.* Fifth Edition. NIH Publication No. 91-3242

- ❖ SEQ ID NOS:125, 693 and 1680 in which there is a cysteine residue prior to amino acid no. 23 in addition to the cysteine at amino acid no. 23; and

- ❖ SEQ ID NO:1554 in which the first cysteine residue is not found until amino acid position no. 89. However, if one examines the region where one expects to find the cysteine residue defined by Kabat-Wu numbering as position number 23, there is a tryptophan residue. Tryptophan is encoded by a codon that shares third position wobble with the codons encoding cysteine residues. The absence of a cysteine residue in this case at Kabat-Wu position no. 23, might be explained by a mutation from the germline sequence; or, more likely - the absence of a cysteine residue at Kabat Wu position No. 23 in SEQ ID NO:1554, is best explained by the presence of a sequencing error because the cysteine residue at position no. 23 is important for the tertiary structure of the variable regions. Absence of this cysteine is apt to disrupt the tertiary structure required by the scFv to bind antigen.

17. Column 5 of the Table in Exhibit E shows the number of amino acids after the $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in the VL region and column 6 of the Table in Exhibit E shows the identity of the amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in the VL region. In 99% (1301/1308) of cases where there are extra amino acids after the $(Gly_4Ser)_3$ sequence, the identity of the amino acids is A, AL or AF. These results indicate that these amino acids most likely arose as a "side-effect" of the cloning strategy used to create the scFvs constructs in the initial generation of the scFv library and further confirm that these residues are not part of the VL region of these scFvs of SEQ ID NOS:2128.

18. Additionally, in some cases where the closest germline gene in V2-13, the first amino acid residue of the VL is calculated to be the last serine residue of the $(Gly_4Ser)_3$ sequence (see, for example, SEQ ID NOS: 4 and 5[3] for which Column 5 of

[3] The following is a complete list of the 238 SEQ ID NOS cases where the closest germline gene is V2-13 and the first amino acid residue of the VL is calculated to be the last serine residue of the $(Gly_4Ser)_3$ sequence: 4, 5, 397, 512, 834, 835, 842, 848, 850, 851, 877, 892, 893, 896, 900, 908, 911, 912, 913, 914,

Exhibit E shows a −1 value). Note that the first amino acid residue of the germline V2-13 residue in Exhibit D is a Serine. Again, this result indicates that in cloning the scFvs to make the original scFv library, a cloning strategy was used that was able to take advantage of the fact that the last amino acid of the $(Gly_4Ser)_3$ sequence could also serve as the first amino acid residue of the VL region[4].

SUMMARY

19. On or before June 16, 2000, an antibody scientist examining the information presented in Table 1 and the sequences of SEQ ID NOS:1-2128 of the Sequence Listing of the '748 patent would have readily recognized that in several instances, the amino acid residues defined in Table 1 as making up the VL region of certain scFvs were incorrect for either containing a few additional amino acids 5' of the VL region or for lacking an amino acid at the 5' end of the VL-region. Moreover, an antibody scientist would have had no difficulty in identifying the correct amino acid residue that corresponded to the first amino acid residue of the VL region.

20. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of

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916, 920, 924, 927, 928, 937, 938, 943, 946, 948, 949, 950, 952, 953, 957, 959, 963, 965, 967, 970, 974, 980, 982, 984, 987, 993, 996, 997, 999, 1050, 1054, 1056, 1065, 1102, 1105, 1108, 1109, 1110, 1111, 1112, 1113, 1115, 1116, 1117, 1118, 1119, 1120, 1170, 1178, 1179, 1181, 1182, 1189, 1192, 1198, 1290, 1293, 1294, 1299, 1300, 1303, 1305, 1306, 1307, 1308, 1315, 1316, 1322, 1323, 1328, 1330, 1331, 1335, 1341, 1344, 1346, 1357, 1367, 1370, 1384, 1386, 1387, 1388, 1391, 1393, 1394, 1402, 1416, 1417, 1424, 1425, 1426, 1433, 1438, 1444, 1445, 1470, 1472, 1474, 1588, 1594, 1596, 1609, 1615, 1620, 1621, 1622, 1623, 1624, 1628, 1638, 1639, 1641, 1643, 1646, 1647, 1648, 1651, 1652, 1655, 1657, 1660, 1662, 1665, 1667, 1668, 1670, 1675, 1676, 1678, 1679, 1681, 1692, 1694, 1702, 1703, 1705, 1708, 1718, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1734, 1740, 1741, 1742, 1755, 1761, 1762, 1764, 1765, 1777, 1781, 1785, 1786, 1788, 1790, 1816, 1817, 1818, 1823, 1826, 1871, 1873, 1877, 1907, 1911, 1912, 1914, 1919, 1924, 1929, 1931, 1937, 1938, 1939, 1940, 1941, 1942, 1944, 1947, 2006, 2008, 2010, 2013, 2014, 2015, 2018, 2021, 2022, 2023, 2031, 2032, 2033, 2035, 2036, 2038, 2039, 2046, 2056, 2057, 2058, 2060, 2066, 2067, 2068, 2106, 2107, 2112,

[4] It is also noted that SEQ ID NO:1389 is another sequence in which , the first amino acid residue of the VL is calculated to be the last serine residue of the $(Gly_4Ser)_3$ sequence. SEQ ID NO:1389 is most closely related to germline V1-13 which begins with a Q amino acid residue. It is likely that the sequence of this VL region was mutated either prior to being cloned into an scFv construct or during passaging or selection of the scFv library.

Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application captioned above or any patent issuing thereupon.

Date: Dec. 14, 2004

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RESEARCH SCIENTIST

QUALIFICATIONS

- Ph.D. in Molecular Biology with 14 years of industrial laboratory experience.
- □ench scientist with expertise in phage antibody display technology, therapeutic antibody generation and characterization, in vitro assay development, protein purification and gene cloning and expression.
- Laboratory and project management experience.

PROFESSIONAL EXPERIENCE

Human Genome Sciences, Inc., Rockville, MD

Senior Scientist I, Antibody Development **08/2002-present**

- Lead scientist for project involved in the discovery and development of therapeutic antibodies to protective antigens from anthrax and plague causing organisms.
- Developed cloning protocols and selection techniques for affinity maturation of scFv's by phage display.
- Generated large panels of specific binding scFv's to a number of soluble and membrane-associated therapeutic target proteins.
- Developed a variety of electrochemiluminescent-based and cell-based assays to identify and characterize lead candidate therapeutic scFv's and/or IgG's.
- Project manager for outside collaboration focused on the discovery of therapeutic antibodies to 7TM chemokine receptors using human Fab phage display libraries.

Scientist, Antibody Development **04/2000-07/2002**

- Developed expression constructs and purification methods for producing homo-trimeric and heterotrimeric forms of BlyS and APRIL.
- Developed novel electrochemiluminescent-based assays to evaluate specificity and affinity of antibodies to a G protein-coupled receptor.
- Engineered mammalian antibody expression vectors to streamline cloning of V-domains and enhance expression of IgG.
- Developed methods for epitope mapping of recombinant antibodies using peptide phage display technology.
- Generated assay reagents and developed assay protocols for evaluating immunogenicity and pK of therapeutic antibodies.

- Generated a panel of fully human IgG's that blocked the catalytic activity of a novel angiotensin converting enzyme.

Bioveris Corp. (formerly IGEN International, Inc.), Gaithersburg, MD

Scientist 3, Assay Development **01/1999 – 04/2000**

- Manager for laboratory focused on the production, purification and validation of antibody and protein reagents used in diagnostic assay development.
- Developed and produced diagnostic and therapeutic antibody reagents on a contract basis using a large human repertoire phage antibody display library.
- Engineered a phage antibody display vector for production of novel binding reagents such as bivalent single-chain antibodies.

Scientist 1 and 2, Molecular Biology / Molecular Engineering **1990 to 1998**

- Principal Investigator (Phase I SBIR) for project focused on constructing a large human repertoire phage antibody display library. Responsibilities included project management, bench research and report writing.
- Optimized primer design, PCR conditions and cDNA cloning methods for generating large human and murine antibody repertoire phage display libraries.
- Coordinated research collaboration involving application of phage antibody display to isolate human and mouse single-chain antibodies with catalytic activity.
- Developed humanized single-chain and bivalent single-chain antibodies for tumor targeting and prodrug activation.
- Developed a bacterial cloning and expression system for high-level production of single-chain antibodies.
- Performed site-directed mutagenesis of an antibody enzyme (abzyme) to delineate catalytic residues.

SUMMARY OF LABORATORY EXPERTISE

Recombinant DNA methods:
mRNA isolation, RT-PCR, 5' RACE, cDNA cloning, vector construction, phage display library construction, site-directed mutagenesis, Northern and Southern hybridization, DNA sequencing, gene transfection, DNA replication assays, DNA diagnostic assays
Protein methods:
Protein Purification (FPLC and BioCad instrumentation), BIAcore analysis, antibody affinity measurements, immunoassay development, SDS-PAGE and Western blotting
Other skills:
Phage display technology, hybridoma production and screening, cell transfection and tissue culture, large scale bacterial fermentation and protein production

EDUCATION

1989 - Ph.D. in Microbiology (Molecular Biology), University of Illinois at Urbana-Champaign. Thesis research in the laboratory of Dr. Edward Voss studying the molecular basis of autoimmunity and anti-DNA autoantibodies in a murine model.

1984 - M.S. in Microbiology, University of Illinois at Urbana-Champaign.
Thesis research in the laboratory of Dr. John Scott studying yeast DNA replication enzymes associated with the chromatin of a freely replicating yeast DNA plasmid.

1981- B.S. in Microbiology, Pennsylvania State University, University Park. Cooperative Study for one year in the Microbiology Research Department at Hershey Foods, Inc., Hershey, PA.

GRANTS AND AWARDS

Phase I Small Business Innovation Research (SBIR) grant ($100,000).
Project Title-Construction of a Large Semi-Synthetic Human Phage Antibody Display Library, 1997. Granting Agency: Dept. of the Army.

U.S. Public Health Service Traineeship, 1984-1987, University of Illinois, awarded for academic achievement.

Clark Microbiology Award, 1983, 1988 and 1989, University of Illinois, for excellence in teaching.

ISSUED PATENTS

Reaction-Based Selection for Expression of and Concentration of Catalytic Moieties
US Patent Number 6,121,007 Date: Sept. 19, 2000 and 6,177,270B1 Date: Jan. 23, 2001

Cycling DNA/RNA Amplification Electrochemiluminescent Assay
US Patent Number 6,048,687 Date: April 11, 2000

The Isolation and Production of Catalytic Antibodies Using Phage Technology
European Patent Number P09002EPO Date: March 14, 2000

Prodrugs Activated by Targeted Catalytic Proteins
US Patent Number 6,258,360 B1 Date: July 10, 2001

Several Additional Patents Pending

PUBLICATIONS AND RECENT ABSTRACTS

1. Baker, K., Edwards, B., Main, H., Choi, G., Wager, R., Halpern, W., Lappin, P., Riccobene, T., Abramian, D., Sekut, L., Sturm, B., Poortman, C., Minter R., Dobson, C., Williams, E., Carmen, S., **Smith, R.**, Roschke, V., Hilbert, D., Vaughan, T., Albert, V. 2003. Generation and characterization of LymphoStat-B, a human monoclonal antibody that antagonizes the bioactivities of B lymphocyte stimulator. *Arthritis Rheum.* **48** (11), 3253-3265.

2. Huang, L., Sexton, D., Skogerson, K., Devlin, M., **Smith, R.**, Sanyal, I., Parry, T., Kent, R., Enright, J., Wu, Q., Conley, G., DeOliveira, D., Morganelli, L., Ducar, M., Wescott, C. and Ladner, R. 2003. Novel Peptide Inhibitors of Angiotensin-converting Enzyme 2. J. Biol. Chem. 278: 15532 - 15540.

3. Roschke, V., Sosnovtseva, S., Ward, C., Hong, J., **Smith, R.**, Albert, V., Stohl, W., Baker, K., Ullrich, S., Nardelli, B., Hilbert, D. and Migone, T. 2002. BlyS and APRIL form biologically active heterotrimers in patients with systemic immune-based rheumatic diseases. *Journal of Immunology* **169**, 4314-4321.

4. Abraham, R., Buxbaum, S., Link, J., **Smith, R.**, Venti, C. and Darsley, M. 1996. Determination of binding constants of diabodies directed against prostate-specific antigen using electrochemiluminescence-based immunoassays. *J. Mol. Recog*. **9**, 456 - 461.

5. **Smith, R.**, Martin, M., Sanchez, R. and Kenten, J. 1995. Cloning and bacterial expression of an esterolytic sFv. *Meth. in Mol. Bio.* **51**, Antibody Engineering Protocols, S. Paul, editor, 297 - 317.

6. Abraham, R., Buxbaum, S., Link, J., **Smith, R.**, Venti, C. and Darsley, M. 1995. Screening and kinetic analysis of recombinant anti-CEA antibody fragments. *J. Imm. Meth.* **183**, 119 -125.

7. McCafferty, J., Fitzgerald, K. J., Earnshaw, J., Chiswell, D. J., Link, J., **Smith, R.** and Kenten, J. 1994. Selection and rapid purification of murine antibody fragments that bind a transition-state analog by phage display. *ABAB* 47, 157-174.

8. Gulliver, G., Bedzyk, W., **Smith, R.**, Bode, S., Tetin, S. and Voss, E. 1994. Conversion of an anti-single-stranded DNA active site to an anti-fluorescein active site through heavy chain complementarity determining region transplantation. *JBC* **269**, 7934.

9. Angeles, T., **Smith, R.,** Darsley, M., Sugasawara, R., Sanchez, R., Kenten, J., Schultz, P. and Martin, M. 1993. Isoabzymes: Structurally and mechanistically similar catalytic antibodies from the same immunization. *Biochemistry* **32**, 12128 -12135.

10. Kenten, J. and **Smith, R.** 1992. Catalytic antibodies from production to application. *Current Opinion in Therapeutic Patents* **2,** 669 -677.

11. **Smith, R.** and Voss, E. 1989. Variable region primary structures of monoclonal anti-DNA autoantibodies from NZB/NZW F1 mice. *Molecular Immunology* **27,** 463 -470.

12. **Smith, R.,** Ballard, D., Blier, P., Pace, P., Bothwell, A., Herron, J., Edmundson, A. and Voss, E. 1989. Structural features of a murine monoclonal anti-ssDNA autoantibody. *J. Ind Inst. of Sci.* **69,** 25-46.

Poster Presentation at ICAAC, Sept. 13, 2003

Selection of Potent Neutralizing Human Monoclonal Antibodies to Protective Antigen of *Bacillus anthracis*. X. Zhang, J. Askins, R. Fleming, B. Sturm, C. Poortman, P. Viriassov, B. Peterson, M. Flynn, Y. Miao, D. Zukauskas, **R. Smith**, M. Laird, G. Choi. Human Genome Sciences, Inc. Rockville, MD

Scheduled for Poster Presentation at ASM, May 26, 2004

Development and Characterization of Fully Human anti-F1 Antibodies that Protect Against Lethal Challenge with *Yersinia pestis* in a Surrogate Mouse Model of Bubonic Plague. R.Fleming[1], D. Zukauskas[1], H. Heine[2], G. Andrews[2], S. Welkos[2], J. Adamovicz[2], M. Laird[1], G. Choi[1], **R. Smith[1]**

[1]Human Genome Sciences, Inc. Rockville, MD, [2]USAMRIID,Frederick, MD

NCBI IgBLAST

Ig Germline Genes

Our collections of germline V genes include functional V genes and V genes with Open Reading Frame (ORF) for the heavy chain, the kappa light chain and the lambda light chain from human and mouse. However, no attempt was made to include all polymorphic forms of germline genes (one should instead search the nr or Ig sequences database for germline gene polymorphism).

In compiling the germline gene sequences, we have retained the nomenclature by the original authors, but we have excluded the signal peptide sequences and the recombination signal sequences. Amino acid sequences are translated in some cases where only nucleotide sequence records are available in GenBank.

Select the germline genes you want to view:
Get sequences

Organism human
Locus VK
Sequence type protein

Although the human Ig kappa locus has not been fully sequenced yet, all of individual genes are likely to have been isolated (Schable KF and Zachau HG, 1993; Brensing-Kuppers J. et al, 1997). The following sequences are taken from these studies.

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Total number of sequences: 46

>A1
DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWD
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP

>A10
EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQSFSGVPS
RFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP

>A11
EIVLTQSPATLSLSPGERATLSCGASQSVSSSYLAWYQQKPGLAPRLLIYDASSRATGIP
DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP

>A14
DVVMTQSPAFLSVTPGEKVTITCQASEGIGNYLYWYQQKPDQAPKLLIKYASQSISGVPS
RFSGSGSGTDFTFTISSLEAEDAATYYCQQGNKHP

>A17
DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP

>A18
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQSPQLLIYEVSSRF
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIHLP

>A19
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

>A2
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRF
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLP

>A20
DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAP

>A23
DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRF
SGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFP

>A26
EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQSFSGVPS
RFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
```

>A27
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP

>A3
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP

>A30
DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP

>A5
EIVMTQTPLSLSITPGEQASISCRSSQSLLHSDGYTYLYWFLQKARPVSTLLIYEVSNRF
SGVPDRFSGSGSGTDFTLKISRVEAEDFGVYYCMQDAQDPP

>A7
DIVMTQTPLSSPVTLGQPASISFRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKVSNRF
SGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCTQATQFP

>B2
ETTLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQQKPGEAAIFIIQEATTLVPGIPP
RFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP

>B3
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP

>L1
DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP

>L10
EIVMTQSPPTLSLSPGERVTLSCRASQSVSSSYLTWYQQKPGQAPRLLIYGASTRATSIP
ARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDHNLPP

>L11
AIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYP

>L12
DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASSLESGVPS
RFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYS

>L14
NIQMTQSPSAMSASVGDRVTITCRARQGISNYLAWFQQKPGKVPKHLIYAASSLQSGVPS
RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP

>L15
DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP

>L16
EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP

>L18
AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQFNNYP

>L19
DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP

>L2
EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP

>L20
EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA
RFSGSGPGTDFTLTISSLEPEDFAVYYCQQRSNWH

>L22
DIQMIQSPSFLSASVGDRVSIICWASEGISSNLAWYLQKPGKSPKLFLYDAKDLHPGVSS
RFSGRGSGTDFTLTIISLKPEDFAAYYCKQDFSYPP

>L23
AIRMTQSPFSLSASVGDRVTITCWASQGISSYLAWYQQKPAKAPKLFIYYASSLQSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYYCQQYYSTP

>L24
VIWMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS
RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFP

>L25
EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKPGQAPRLLIYGASTRATGIP
ARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDYNLP

>L4/18a
AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYP

>L5
DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP

>L6
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA
RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP

>L8
DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPS
RFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSYP

>L9
AIRMTQSPSSFSASTGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPS
RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSYP

>O1
DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLLIYTLSYR
ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP

>O11
DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLLIYTLSYR
ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP

>O12
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP

>O14
DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNLQSGVPS
RFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP

>O18
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP

>O2
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP

>O4
DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNLQSGVPS
RFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP

>O8
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP

The following sequences are taken from a study that has sequenced the entire human lambda gene locus (Kawasaki K. et al, 1997).

Total number of sequences: 36

>V1-11
QSVLTQPPSVSEAPRQRVTISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYYDDLLPSGVS
DRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP

>V1-13
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGV
PDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGS

>V1-16
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSGVP
DRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP

>V1-17
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNNQRPSGVP
DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGP

>V1-18
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYVVHWYQQLPGTAPKLLIYGNSNRPSGV
PDQFSGSKSGTSASLAITGLQSEDEADYYCKAWDNSLNA

>V1-19
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP
DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAG

>V1-2
QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEVSKRPSGV
PDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGSNNF

>V1-20
QAGLTQPPSVSKGLRQTATLTCTGNSNIVGNQGAAWLQQHQGHPPKLLSYRNNNRPSGIS
ERFSASRSGNTASLTITGLQPEDEADYYCSALDSSLSA

>V1-22
NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYEDNQRPSGVP
DRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSN

>V1-3
QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSKRPSGV
PDRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSYTF

>V1-4
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYEVSNRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTL

>V1-5
QSALTQPPSVSGSPGQSVTISCTGTSSDVGSYNRVSWYQQPPGTAPKLMIYEVSNRPSGV
PDRFSGSKSGNTASLTISGLQAEDEADYYCSLYTSSSTF

>V1-7
QSALTQPASVSGSPGQSITISCTGTSSDVGSYNLVSWYQQHPGKAPKLMIYEGSKRPSGV
SNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTF

>V1-9
QSALTQPPFVSGAPGQSVTISCTGTSSDVGDYDHVFWYQKRLSTTSRLLIYNVNTRPSGI
SDLFSGSKSGNMASLTISGLKSEVEANYHCSLYSSSYTF

>V2-1
SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQSPVLVIYQDSKRPSGIPER
FSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTA

>V2-11
SYELTQPPSVSVSLGQMARITCSGEALPKKYAYWYQQKPGQFPVLVIYKDSERPSGIPER
FSGSSSGTIVTLTISGVQAEDEADYYCLSADSSGTYP

>V2-13
SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR
FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHL

>V2-14
SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPSGIPER
FSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHP

>V2-15
SYELTQLPSVSVSPGQTARITCSGDVLGENYADWYQQKPGQAPELVIYEDSERYPGIPER
FSGSTSGNTTTLTISRVLTEDEADYYCLSGDEDNP

>V2-17
SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDSERPSGIPER
FSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYP

>V2-19
SYELTQPSSVSVSPGQTARITCSGDVLAKKYARWFQQKPGQAPVLVIYKDSERPSGIPER
FSGSSSGTTVTLTISGAQVEDEADYYCYSAADNNL

>V2-6
SYELTQPLSVSVALGQTARITCGGNNIGSKNVHWYQQKPGQAPVLVIYRDSNRPSGIPER
FSGSNSGNTATLTISRAQAGDEADYYCQVWDSSTA

>V2-7
SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKSGQAPVLVIYEDSKRPSGIPER
FSGSSSGTMATLTISGAQVEDEADYYCYSTDSSGNH

>V2-8
SYELTQPHSVSVATAQMARITCGGNNIGSKAVHWYQQKPGQDPVLVIYSDSNRPSGIPER
FSGSNPGNTATLTISRIEAGDEADYYCQVWDSSSDHP

>V3-2
QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGYYPNWFQQKPGQAPRALIYSTSNKHSWT
PARFSGSLLGGKAALTLSGVQPEDEAEYYCLLYYGGAQ

>V3-3
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYPYWFQQKPGQAPRTLIYDTSNKHSWT
PARFSGSLLGGKAALTLLGAQPEDEAEYYCLLSYSGAR

>V3-4
QTVVTQEPSFSVSPGGTVTLTCGLSSGSVSTSYYPSWYQQTPGQAPRTLIYSTNTRSSGV
PDRFSGSILGNKAALTITGAQADDESDYYCVLYMGSGIS

>V4-1
QPVLTQPPSSSASPGESARLTCTLPSDINVGSYNIYWYQQKPGSPPRYLLYYYSDSDKGQ
GSGVPSRFSGSKDASANTGILLISGLQSEDEADYYCMIWPSNAS

>V4-2
QAVLTQPSSLSASPGASASLTCTLRSGINVGTYRIYWYQQKPGSPPQYLLRYKSDSDKQQ
GSGVPSRFSGSKDASANAGILLISGLQSEDEADYYCMIWHSSAS

>V4-3
QPVLTQPTSLSASPGASARLTCTLRSGINLGSYRIFWYQQKPESPPRYLLSYYSDSSKHQ
GSGVPSRFSGSKDASSNAGILVISGLQSEDEADYYCMIWHSSAS

>V4-4
QPVLTQPSSHSASSGASVRLTCMLSSGFSVGDFWIRWYQQKPGNPPRYLLYYHSDSNKGQ
GSGVPSRFSGSNDASANAGILRISGLQPEDEADYYCGTWHSNSKT

>V4-6
RPVLTQPPSLSASPGATARLPCTLSSDLSVGGKNMFWYQQKPGSSPRLFLYHYSDSDKQL
GPGVPSRVSGSKETSSNTAFLLISGLQPEDEADYYCQVYESSAN

>V5-1
LPVLTQPPSASALLGASIKLTCTLSSEHSTYTIEWYQQRPGRSPQYIMKVKSDGSHSKGD
GIPDRFMGSSSGADRYLTFSNLQSDDEAEYHCGESHTIDGQVG

>V5-2
QPVLTQPPSASASLGASVTLTCTLSSGYSNYKVDWYQQRPGKGPRFVMRVGTGGIVGSKG
DGIPDRFSVLGSGLNRYLTIKNIQEEDESDYHCGADHGSGSNFV

>V5-4
QPVLTQSSSASASLGSSVKLTCTLSSGHSSYIIAWHQQQPGKAPRYLMKLEGSGSYNKGS
GVPDRFSGSSSGADRYLTISNLQFEDEADYYCETWDSNT

>V5-6
QLVLTQSPSASASLGASVKLTCTLSSGHSSYAIAWHQQQPEKGPRYLMKLNSDGSHSKGD
GIPDRFSGSSSGAERYLTISSLQSEDEADYYCQTWGTG

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1	V1-4	lambda	94	0	
2	V2-13	lambda	98	2	AF
3	V1-3	lambda	85	0	
4	V2-13	lambda	98	-1	
5	V2-13	lambda	91	-1	
6	V1-13	lambda	95	1	A
7	V2-13	lambda	94	2	AL
8	V1-4	lambda	100	1	A
9	A27	kappa	84	2	AL
10	A27	kappa	85	2	AL
11	A27	kappa	84	2	AL
12	A27	kappa	85	2	AL
13	A27	kappa	84	2	AL
14	A27	kappa	84	2	AL
15	A27	kappa	84	2	AL
16	A27	kappa	84	2	AL
17	A27	kappa	85	2	AL
18	A27	kappa	84	2	AL
19	A27	kappa	85	2	AL
20	A27	kappa	84	2	AL
21	A27	kappa	85	2	AL
22	A27	kappa	86	2	AL
23	A27	kappa	85	2	AL
24	A27	kappa	86	2	AL
25	A27	kappa	85	2	AL
26	A27	kappa	86	2	AL
27	A27	kappa	85	2	AL
28	A27	kappa	86	2	AL
29	A27	kappa	85	2	AL
30	A27	kappa	86	2	AL
31	A27	kappa	85	2	AL
32	A27	kappa	84	2	AL
33	A27	kappa	85	2	AL
34	A27	kappa	84	2	AL
35	A27	kappa	84	2	AL
36	A27	kappa	84	2	AL
37	A27	kappa	84	2	AL
38	A27	kappa	84	2	AL
39	A27	kappa	85	2	AL
40	A27	kappa	84	2	AL
41	A27	kappa	84	2	AL
42	A27	kappa	84	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
43	A27	kappa	85	2	AL
44	A27	kappa	83	2	AL
45	A27	kappa	84	2	AL
46	A27	kappa	84	2	AL
47	A27	kappa	84	2	AL
48	A27	kappa	84	2	AL
49	A27	kappa	83	2	AL
50	A27	kappa	84	2	AL
51	A27	kappa	84	2	AL
52	A27	kappa	84	2	AL
53	A27	kappa	83	2	AL
54	A27	kappa	84	2	AL
55	A27	kappa	84	2	AL
56	A27	kappa	84	2	AL
57	A27	kappa	84	2	AL
58	A27	kappa	84	2	AL
59	A27	kappa	84	2	AL
60	A27	kappa	83	2	AL
61	A27	kappa	84	2	AL
62	A27	kappa	84	2	AL
63	A27	kappa	84	2	AL
64	A27	kappa	84	2	AL
65	A27	kappa	84	2	AL
66	A27	kappa	83	2	AL
67	A27	kappa	83	2	AL
68	A27	kappa	84	2	AL
69	A27	kappa	84	2	AL
70	A27	kappa	84	2	AL
71	A27	kappa	83	2	AL
72	A27	kappa	84	2	AL
73	A27	kappa	84	2	AL
74	A27	kappa	84	2	AL
75	A27	kappa	84	2	AL
76	A27	kappa	84	2	AL
77	A27	kappa	84	2	AL
78	A27	kappa	84	2	AL
79	A27	kappa	84	2	AL
80	A27	kappa	84	2	AL
81	A27	kappa	84	2	AL
82	A20	kappa	96	0	
83	A27	kappa	83	2	AL
84	A27	kappa	84	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
85	A27	kappa	85	2	AL
86	A27	kappa	84	2	AL
87	A27	kappa	84	2	AL
88	A27	kappa	84	2	AL
89	A27	kappa	84	2	AL
90	A27	kappa	84	2	AL
91	A27	kappa	84	2	AL
92	A27	kappa	84	2	AL
93	A27	kappa	84	2	AL
94	A27	kappa	84	2	AL
95	A27	kappa	84	2	AL
96	A27	kappa	84	2	AL
97	A27	kappa	84	2	AL
98	A27	kappa	84	2	AL
99	A27	kappa	82	2	AL
100	A27	kappa	84	2	AL
101	A27	kappa	84	2	AL
102	A27	kappa	84	2	AL
103	A27	kappa	84	2	AL
104	A27	kappa	83	2	AL
105	A27	kappa	84	2	AL
106	A27	kappa	84	2	AL
107	A27	kappa	84	2	AL
108	A27	kappa	83	2	AL
109	A27	kappa	84	2	AL
110	A27	kappa	85	2	AL
111	A27	kappa	84	2	AL
112	A27	kappa	84	2	AL
113	A27	kappa	84	2	AL
114	A27	kappa	84	2	AL
115	A27	kappa	84	2	AL
116	A27	kappa	83	2	AL
117	A27	kappa	81	2	AL
118	A27	kappa	83	2	AL
119	A27	kappa	84	2	AL
120	A27	kappa	83	2	AL
121	A27	kappa	84	2	AL
122	A27	kappa	84	2	AL
123	A27	kappa	84	2	AL
124	A27	kappa	84	2	AL
125	A27	kappa	83	2	AL
126	A27	kappa	82	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
127	A27	kappa	84	2	AL
128	A27	kappa	86	2	AL
129	A27	kappa	84	2	AL
130	A27	kappa	84	2	AL
131	A27	kappa	84	2	AL
132	A27	kappa	84	2	AL
133	A27	kappa	82	2	AL
134	A27	kappa	83	2	AL
135	A27	kappa	84	2	AL
136	A27	kappa	84	2	AL
137	A27	kappa	83	2	AL
138	A27	kappa	80	2	AL
139	A27	kappa	84	2	AL
140	A27	kappa	84	2	AL
141	A27	kappa	83	2	AL
142	A27	kappa	83	2	AL
143	A27	kappa	84	2	AL
144	A27	kappa	84	2	AL
145	A27	kappa	83	2	AL
146	A27	kappa	84	2	AL
147	A27	kappa	83	2	AL
148	A27	kappa	81	2	AL
149	A27	kappa	84	2	AL
150	A27	kappa	84	2	AL
151	A27	kappa	84	2	AL
152	A27	kappa	84	2	AL
153	A27	kappa	84	2	AL
154	A27	kappa	82	2	AL
155	A27	kappa	84	2	AL
156	A27	kappa	83	2	AL
157	A27	kappa	83	2	AL
158	A27	kappa	84	2	AL
159	A27	kappa	84	2	AL
160	A27	kappa	84	2	AL
161	A27	kappa	84	2	AL
162	A27	kappa	83	2	AL
163	A27	kappa	83	2	AL
164	A20	kappa	96	0	
165	A27	kappa	84	2	AL
166	A27	kappa	84	2	AL
167	A27	kappa	83	2	AL
168	A27	kappa	84	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
169	A27	kappa	83	2	AL
170	A27	kappa	84	2	AL
171	A27	kappa	84	2	AL
172	A27	kappa	84	2	AL
173	A27	kappa	84	2	AL
174	A27	kappa	84	2	AL
175	A27	kappa	82	2	AL
176	A27	kappa	84	2	AL
177	A27	kappa	84	2	AL
178	A27	kappa	85	2	AL
179	A27	kappa	83	2	AL
180	A27	kappa	84	2	AL
181	A27	kappa	84	2	VL
182	A27	kappa	84	2	AL
183	A27	kappa	84	2	AL
184	A27	kappa	84	2	AL
185	A27	kappa	84	2	AL
186	A27	kappa	80	2	AL
187	A27	kappa	76	2	AL
188	A27	kappa	84	2	AL
189	A27	kappa	84	2	AL
190	A27	kappa	84	2	AL
191	A27	kappa	84	2	AL
192	A27	kappa	83	2	AL
193	A27	kappa	84	2	AL
194	A27	kappa	84	2	AL
195	A27	kappa	84	2	AL
196	A27	kappa	81	2	AL
197	A27	kappa	82	2	AL
198	A27	kappa	84	2	AL
199	A27	kappa	84	2	AL
200	A27	kappa	84	2	AL
201	A27	kappa	82	2	AL
202	A27	kappa	83	2	AL
203	A27	kappa	83	2	AL
204	A27	kappa	84	2	AL
205	A27	kappa	83	2	AL
206	A27	kappa	84	2	AL
207	A27	kappa	84	2	AL
208	A27	kappa	84	2	AL
209	A27	kappa	83	2	AL
210	A27	kappa	79	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
211	A27	kappa	84	2	AL
212	A27	kappa	84	2	AL
213	A27	kappa	84	2	AL
214	A27	kappa	83	2	AL
215	A27	kappa	84	2	AL
216	A27	kappa	84	2	AL
217	A27	kappa	84	2	AL
218	A27	kappa	84	2	AL
219	A27	kappa	84	2	AL
220	A27	kappa	84	2	AL
221	A27	kappa	84	2	AL
222	A27	kappa	84	2	AL
223	A27	kappa	83	2	AL
224	A27	kappa	84	2	AL
225	A27	kappa	84	2	AL
226	A27	kappa	84	2	AL
227	A27	kappa	84	2	AL
228	A27	kappa	84	2	AL
229	A27	kappa	83	2	AL
230	A27	kappa	84	2	AL
231	A27	kappa	84	2	AL
232	A27	kappa	84	2	AL
233	A27	kappa	83	2	AL
234	A27	kappa	84	2	AL
235	A27	kappa	84	2	AL
236	A27	kappa	84	2	AL
237	A27	kappa	84	2	AL
238	A27	kappa	84	2	AL
239	A27	kappa	84	2	AL
240	A27	kappa	84	2	AL
241	A27	kappa	84	2	AL
242	A27	kappa	84	2	AL
243	A27	kappa	83	2	AL
244	A27	kappa	84	2	AL
245	A27	kappa	84	2	AL
246	A27	kappa	84	2	AL
247	A27	kappa	84	2	AL
248	A27	kappa	84	2	AL
249	A27	kappa	83	2	AL
250	A27	kappa	84	2	AL
251	A27	kappa	84	2	AL
252	A27	kappa	84	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
253	A27	kappa	83	2	AL
254	A27	kappa	84	2	AL
255	A27	kappa	84	2	AL
256	A27	kappa	84	2	AL
257	A27	kappa	83	2	AL
258	A27	kappa	83	2	AL
259	A27	kappa	84	2	AL
260	A27	kappa	84	2	AL
261	A20	kappa	96	0	
262	A27	kappa	84	2	AL
263	A27	kappa	84	2	AL
264	A27	kappa	84	2	AL
265	A27	kappa	84	2	AL
266	A27	kappa	85	2	AL
267	A27	kappa	83	2	AL
268	A27	kappa	84	2	AL
269	A27	kappa	84	2	AL
270	A27	kappa	84	2	AL
271	A27	kappa	84	2	AL
272	A27	kappa	84	2	AL
273	A27	kappa	84	2	AL
274	A27	kappa	84	2	AL
275	A27	kappa	84	2	AL
276	A27	kappa	84	2	AL
277	A27	kappa	84	2	AL
278	A27	kappa	83	2	AL
279	A27	kappa	83	2	AL
280	A20	kappa	95	0	
281	A27	kappa	83	2	AL
282	A27	kappa	83	2	AL
283	A27	kappa	84	2	AL
284	A27	kappa	83	2	AL
285	A27	kappa	84	2	AL
286	A27	kappa	82	2	AL
287	A27	kappa	83	2	AL
288	A27	kappa	83	2	AL
289	A27	kappa	84	2	AL
290	A27	kappa	84	2	AL
291	A27	kappa	84	2	AL
292	A27	kappa	84	2	AL
293	A27	kappa	84	2	AL
294	A27	kappa	84	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
295	A27	kappa	84	2	AL
296	A27	kappa	84	2	AL
297	A27	kappa	84	2	AL
298	A27	kappa	83	2	AL
299	A27	kappa	84	2	AL
300	A27	kappa	83	2	AL
301	A27	kappa	84	2	AL
302	A27	kappa	84	2	AL
303	A27	kappa	83	2	AL
304	A27	kappa	84	2	AL
305	A27	kappa	84	2	AL
306	A27	kappa	84	2	AL
307	A27	kappa	83	2	AL
308	A27	kappa	85	2	AL
309	A27	kappa	84	2	GL
310	A27	kappa	83	2	AL
311	A27	kappa	84	2	AL
312	A27	kappa	84	2	AP
313	A27	kappa	84	2	AL
314	A27	kappa	82	2	AL
315	A27	kappa	82	2	AL
316	A27	kappa	81	2	AL
317	A27	kappa	85	2	AL
318	A27	kappa	84	2	AL
319	A27	kappa	84	2	AL
320	A27	kappa	83	2	AL
321	V2-13	lambda	97	2	AF
322	V2-13	lambda	97	2	AF
323	V2-13	lambda	98	2	AF
324	V2-13	lambda	98	2	AF
325	V2-13	lambda	97	2	AF
326	V2-13	lambda	98	2	AF
327	V2-13	lambda	97	2	AF
328	V2-13	lambda	97	2	AF
329	V2-13	lambda	97	2	AF
330	V2-13	lambda	97	2	AF
331	V2-13	lambda	97	2	AF
332	V2-13	lambda	98	2	AF
333	V2-13	lambda	98	2	AF
334	V2-13	lambda	98	2	AF
335	V2-13	lambda	98	2	AF
336	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
337	V2-13	lambda	97	2	AF
338	V2-13	lambda	98	2	AF
339	V2-13	lambda	98	2	AF
340	V2-13	lambda	95	2	AF
341	V2-13	lambda	98	2	AS
342	V2-13	lambda	98	2	AF
343	V2-13	lambda	98	2	AF
344	V2-13	lambda	98	2	AF
345	V2-13	lambda	98	2	AF
346	V2-13	lambda	97	2	AF
347	V2-13	lambda	98	2	AF
348	V2-13	lambda	98	2	AF
349	V2-13	lambda	98	2	AF
350	V2-13	lambda	98	2	AF
351	V2-13	lambda	97	2	AF
352	V2-13	lambda	98	2	AF
353	V2-13	lambda	96	2	AF
354	V2-13	lambda	98	2	AF
355	V2-13	lambda	98	2	AF
356	V2-13	lambda	98	2	AF
357	V2-13	lambda	98	2	AF
358	V2-13	lambda	98	2	AF
359	V2-13	lambda	98	2	AF
360	V2-13	lambda	98	2	AF
361	V2-13	lambda	98	2	AF
362	V2-13	lambda	97	2	AF
363	V2-13	lambda	98	2	AF
364	V2-13	lambda	98	2	AF
365	V2-13	lambda	98	2	AF
366	V2-13	lambda	98	2	AS
367	V2-13	lambda	98	2	AF
368	V2-13	lambda	98	2	AF
369	V2-13	lambda	98	2	AF
370	V2-13	lambda	98	2	AF
371	V2-13	lambda	98	2	AF
372	V2-13	lambda	98	2	AF
373	V2-13	lambda	98	2	AF
374	V2-13	lambda	97	2	AF
375	V2-13	lambda	98	2	AF
376	V2-13	lambda	98	2	AF
377	V2-13	lambda	98	2	AF
378	V2-13	lambda	97	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X.	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
379	V2-13	lambda	98	2	AF
380	V2-13	lambda	97	2	AF
381	V2-13	lambda	98	2	AF
382	V2-13	lambda	98	2	AF
383	V2-13	lambda	98	2	AF
384	V2-13	lambda	97	2	AF
385	V2-13	lambda	98	2	AF
386	V2-13	lambda	98	2	AF
387	V2-13	lambda	98	2	AF
388	V2-13	lambda	98	2	AF
389	V2-13	lambda	97	2	AF
390	V2-13	lambda	98	2	AF
391	V2-13	lambda	98	2	AF
392	V2-13	lambda	98	2	AF
393	V2-13	lambda	98	2	AF
394	V2-13	lambda	97	2	AF
395	V2-13	lambda	98	2	AF
396	V2-13	lambda	98	2	AF
397	V2-13	lambda	91	-1	
398	V2-13	lambda	98	2	AF
399	V2-13	lambda	98	2	AF
400	V2-13	lambda	98	2	AF
401	V2-13	lambda	97	2	AF
402	V2-13	lambda	98	2	AF
403	V2-13	lambda	98	2	AF
404	V2-13	lambda	98	2	AF
405	V2-13	lambda	98	2	AF
406	V2-13	lambda	98	2	AF
407	V2-13	lambda	97	2	AF
408	V2-13	lambda	98	2	AF
409	V2-13	lambda	98	2	AF
410	V2-13	lambda	98	2	AF
411	V2-13	lambda	98	2	AF
412	V2-13	lambda	98	2	AF
413	V2-13	lambda	98	2	AF
414	V2-13	lambda	98	2	AF
415	V2-13	lambda	98	2	AF
416	V2-13	lambda	98	2	AF
417	V2-13	lambda	98	2	AF
418	V2-13	lambda	98	2	AF
419	V2-13	lambda	98	2	AF
420	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after (Gly4Ser)3 sequence prior to amino acid position no 1 in VL region	Identity of amino acids after (Gly4Ser)3 sequence prior to amino acid position no. 1 in VL region
421	V2-13	lambda	98	2	AF
422	V2-13	lambda	98	2	AF
423	V2-13	lambda	97	2	AF
424	V2-13	lambda	98	2	AF
425	V2-13	lambda	97	2	AF
426	V2-13	lambda	98	2	AF
427	V2-13	lambda	98	2	AF
428	V2-13	lambda	98	2	AF
429	V2-13	lambda	98	2	AF
430	V2-13	lambda	98	2	AF
431	V2-13	lambda	98	2	AF
432	V2-13	lambda	98	2	AF
433	V2-13	lambda	98	2	AF
434	V2-13	lambda	97	2	AF
435	V2-13	lambda	98	2	AF
436	V2-13	lambda	97	2	AF
437	V2-13	lambda	98	2	AF
438	V2-13	lambda	97	2	AF
439	V2-13	lambda	98	2	AF
440	V2-13	lambda	98	2	AF
441	V2-13	lambda	97	2	AF
442	V2-13	lambda	98	2	AF
443	V2-13	lambda	98	2	AF
444	V2-13	lambda	98	2	AF
445	V2-13	lambda	98	2	AF
446	V2-13	lambda	98	2	AF
447	V2-13	lambda	97	2	AF
448	V2-13	lambda	98	2	AF
449	V2-13	lambda	98	2	AF
450	V2-13	lambda	98	2	AF
451	V2-13	lambda	97	2	AF
452	V2-13	lambda	98	2	AF
453	V2-13	lambda	97	2	AF
454	V2-13	lambda	98	2	AF
455	V2-13	lambda	98	2	AF
456	V2-13	lambda	97	2	AF
457	V2-13	lambda	98	2	AF
458	V2-13	lambda	98	2	AF
459	V2-13	lambda	98	2	AF
460	V2-13	lambda	97	2	AF
461	V2-13	lambda	98	2	AF
462	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
463	V2-13	lambda	98	2	AF
464	V2-13	lambda	98	2	AF
465	V2-13	lambda	98	2	AF
466	V2-13	lambda	98	2	AF
467	V2-13	lambda	98	2	AF
468	V2-13	lambda	98	2	AF
469	V2-13	lambda	98	2	AF
470	V2-13	lambda	98	2	AF
471	V2-13	lambda	97	2	AF
472	V2-13	lambda	98	2	AF
473	V2-13	lambda	97	2	AF
474	V2-13	lambda	98	2	AF
475	V2-13	lambda	98	2	AF
476	V2-13	lambda	98	2	AF
477	V2-13	lambda	98	2	AF
478	V2-13	lambda	98	2	AF
479	V2-13	lambda	97	2	AF
480	V2-13	lambda	96	2	AF
481	V2-13	lambda	98	2	AF
482	V2-13	lambda	98	2	AF
483	V2-13	lambda	98	2	AF
484	V2-13	lambda	96	2	AF
485	V2-13	lambda	98	2	AF
486	V2-13	lambda	98	2	AF
487	V2-13	lambda	98	2	AF
488	V2-13	lambda	98	2	AF
489	V2-13	lambda	98	2	AF
490	V2-13	lambda	98	2	AF
491	V2-13	lambda	98	2	AF
492	V2-13	lambda	98	2	AF
493	V2-13	lambda	97	2	AF
494	V2-13	lambda	98	2	AF
495	V2-13	lambda	98	2	AF
496	V2-13	lambda	98	2	AF
497	V2-13	lambda	98	2	AF
498	V2-13	lambda	98	2	AF
499	V2-13	lambda	98	2	AF
500	V2-13	lambda	98	2	AF
501	V2-13	lambda	98	2	AF
502	V2-13	lambda	98	2	AF
503	V2-13	lambda	97	2	AF
504	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
505	V2-13	lambda	98	2	AF
506	V2-13	lambda	97	2	AF
507	V2-13	lambda	98	2	AF
508	V2-13	lambda	98	2	AF
509	V2-13	lambda	98	2	AF
510	V2-13	lambda	98	2	AF
511	V2-13	lambda	98	2	AF
512	V2-13	lambda	91	-1	
513	V2-13	lambda	98	2	AF
514	V2-13	lambda	98	2	AF
515	V2-13	lambda	98	2	AF
516	V2-13	lambda	98	2	AF
517	V2-13	lambda	98	2	AF
518	V2-13	lambda	98	2	AF
519	V2-13	lambda	98	2	AF
520	V2-13	lambda	98	2	AF
521	V2-13	lambda	98	2	AF
522	V2-13	lambda	98	2	AF
523	V2-13	lambda	98	2	AF
524	V2-13	lambda	97	2	AF
525	V2-13	lambda	98	2	AF
526	V2-13	lambda	98	2	AF
527	V2-13	lambda	98	2	AF
528	V2-13	lambda	98	2	AF
529	V2-13	lambda	98	2	AF
530	V2-13	lambda	98	2	AF
531	V2-13	lambda	97	2	AF
532	V2-13	lambda	98	2	AF
533	V2-13	lambda	98	2	AF
534	V2-13	lambda	98	2	AF
535	V2-13	lambda	98	2	AF
536	V2-13	lambda	98	2	AF
537	V2-13	lambda	98	2	AF
538	V2-13	lambda	98	2	AF
539	V2-13	lambda	98	2	AF
540	V2-13	lambda	96	2	AF
541	V2-13	lambda	97	2	AF
542	V2-13	lambda	98	2	AF
543	V2-13	lambda	98	2	AF
544	V2-13	lambda	97	2	AF
545	V2-13	lambda	98	2	AF
546	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
547	V2-13	lambda	98	2	AF
548	V2-13	lambda	98	2	AF
549	V2-13	lambda	98	2	AF
550	V2-13	lambda	97	2	AF
551	V2-13	lambda	98	2	AF
552	V2-13	lambda	98	2	AF
553	V2-13	lambda	98	2	AF
554	V2-13	lambda	98	2	AF
555	V2-13	lambda	98	2	AF
556	V2-13	lambda	98	2	AF
557	V2-13	lambda	98	2	AF
558	V2-13	lambda	98	2	AF
559	V2-13	lambda	98	2	AF
560	V2-13	lambda	98	2	AF
561	V2-13	lambda	98	2	AF
562	V2-13	lambda	98	2	AF
563	V2-13	lambda	97	2	AF
564	V2-13	lambda	98	2	AF
565	V2-13	lambda	98	2	AF
566	V2-13	lambda	98	2	AF
567	V2-13	lambda	98	2	AF
568	V2-13	lambda	98	2	AF
569	V2-13	lambda	98	2	AF
570	V2-13	lambda	98	2	AF
571	V2-13	lambda	97	2	AF
572	V2-13	lambda	98	2	AF
573	V2-13	lambda	98	2	AF
574	V2-13	lambda	98	2	AF
575	V2-13	lambda	98	2	AF
576	V2-13	lambda	98	2	AF
577	V2-13	lambda	98	2	AF
578	V2-13	lambda	97	2	AF
579	V2-13	lambda	98	2	AF
580	V2-13	lambda	98	2	AF
581	V2-13	lambda	98	2	AF
582	V2-13	lambda	98	2	AF
583	V2-13	lambda	98	2	AF
584	V2-13	lambda	98	2	AF
585	V2-13	lambda	98	2	AF
586	V2-13	lambda	98	2	AF
587	V2-13	lambda	98	2	AF
588	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
589	V2-13	lambda	98	2	AF
590	V2-13	lambda	98	2	AF
591	V2-13	lambda	98	2	AF
592	V2-13	lambda	98	2	AF
593	V2-13	lambda	98	2	AF
594	V2-13	lambda	98	2	AF
595	V2-13	lambda	97	2	AF
596	V2-13	lambda	98	2	AF
597	V2-13	lambda	98	2	AF
598	V2-13	lambda	98	2	AF
599	V2-13	lambda	98	2	AF
600	V2-13	lambda	97	2	AF
601	V2-13	lambda	98	2	AF
602	V2-13	lambda	98	2	AF
603	V2-13	lambda	98	2	AF
604	V2-13	lambda	98	2	AF
605	V2-13	lambda	98	2	AF
606	V2-13	lambda	98	2	AF
607	V2-13	lambda	98	2	AF
608	V2-13	lambda	98	2	AF
609	V2-13	lambda	98	2	AF
610	V2-13	lambda	98	2	AF
611	V2-13	lambda	98	2	AF
612	V2-13	lambda	96	2	AF
613	V2-13	lambda	98	2	AF
614	V2-13	lambda	98	2	AF
615	V2-13	lambda	98	2	AF
616	V2-13	lambda	97	2	AF
617	V2-13	lambda	98	2	AF
618	V2-13	lambda	97	2	AF
619	V2-13	lambda	98	2	AF
620	V2-13	lambda	96	2	AF
621	V2-13	lambda	98	2	AF
622	V2-13	lambda	98	2	AF
623	V2-13	lambda	98	2	AF
624	V2-13	lambda	98	2	AF
625	V2-13	lambda	97	2	AF
626	V2-13	lambda	97	2	AF
627	V2-13	lambda	98	2	AF
628	V2-13	lambda	97	2	AF
629	V2-13	lambda	98	2	AF
630	V2-13	lambda	97	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
631	V2-13	lambda	98	2	AF
632	V2-13	lambda	98	2	AF
633	V2-13	lambda	98	2	AF
634	V2-13	lambda	98	2	AF
635	V2-13	lambda	98	2	AF
636	V2-13	lambda	97	2	AF
637	V2-13	lambda	98	2	AF
638	V2-13	lambda	98	2	AF
639	V2-13	lambda	98	2	AF
640	V2-13	lambda	97	2	AF
641	V2-13	lambda	97	2	AF
642	V2-13	lambda	98	2	AF
643	V2-13	lambda	97	2	AF
644	V2-13	lambda	98	2	AF
645	V2-13	lambda	98	2	AF
646	V2-13	lambda	98	2	AF
647	V2-13	lambda	98	2	AF
648	V2-13	lambda	98	2	AF
649	V2-13	lambda	98	2	AF
650	V2-13	lambda	98	2	AF
651	V2-13	lambda	98	2	AF
652	V2-13	lambda	98	2	AF
653	V2-13	lambda	98	2	AF
654	V2-13	lambda	98	2	AF
655	V2-13	lambda	98	2	AF
656	V2-13	lambda	97	2	AF
657	V2-13	lambda	98	2	AF
658	V2-13	lambda	98	2	AF
659	V2-13	lambda	98	2	AF
660	V2-13	lambda	98	2	AF
661	V2-13	lambda	98	2	AF
662	V2-13	lambda	98	2	AF
663	V2-13	lambda	98	2	AF
664	V2-13	lambda	97	2	AF
665	V2-13	lambda	97	2	AF
666	V2-13	lambda	98	2	AF
667	V2-13	lambda	98	2	AF
668	V2-13	lambda	98	2	AF
669	V2-13	lambda	98	2	AF
670	V2-13	lambda	98	2	AF
671	V2-13	lambda	98	2	AF
672	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
673	V2-13	lambda	98	2	AF
674	V2-13	lambda	98	2	AF
675	V2-13	lambda	98	2	AF
676	V2-13	lambda	97	2	AF
677	V2-13	lambda	97	2	AF
678	V2-13	lambda	97	2	AF
679	V2-13	lambda	98	2	AF
680	V2-13	lambda	97	2	AF
681	V2-13	lambda	98	2	AF
682	V2-13	lambda	98	2	AF
683	V2-13	lambda	96	2	AF
684	V2-13	lambda	98	2	AF
685	V2-13	lambda	97	2	AF
686	V2-13	lambda	97	2	AF
687	V2-13	lambda	98	2	AF
688	V2-13	lambda	98	2	AF
689	V2-13	lambda	96	2	AF
690	V2-13	lambda	98	2	AF
691	V2-13	lambda	98	2	AF
692	V2-13	lambda	98	2	AF
693	V2-13	lambda	97	2	AF
694	V2-13	lambda	98	2	AF
695	V2-13	lambda	97	2	AF
696	V2-13	lambda	98	2	AF
697	V2-13	lambda	97	2	AF
698	V2-13	lambda	98	2	AF
699	V2-13	lambda	98	2	AF
700	V2-13	lambda	97	2	AF
701	V2-13	lambda	98	2	AF
702	V2-13	lambda	98	2	AF
703	V2-13	lambda	95	2	AF
704	V2-13	lambda	95	2	AF
705	V2-13	lambda	96	2	AF
706	V2-13	lambda	98	2	AF
707	V2-13	lambda	98	2	AF
708	V2-13	lambda	97	2	AF
709	V2-13	lambda	98	2	AF
710	V2-13	lambda	98	2	AF
711	V2-13	lambda	98	2	AF
712	V2-13	lambda	98	2	AF
713	V2-13	lambda	98	2	AF
714	V2-13	lambda	98	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
715	V2-13	lambda	98	2	AF
716	V2-13	lambda	98	2	AF
717	V2-13	lambda	98	2	AF
718	V2-13	lambda	98	2	AF
719	V2-13	lambda	97	2	AF
720	V2-13	lambda	96	2	AF
721	V2-13	lambda	98	2	AF
722	V2-13	lambda	98	2	AF
723	V2-13	lambda	97	2	AF
724	V2-13	lambda	98	2	AF
725	V2-13	lambda	98	2	AF
726	V2-13	lambda	98	2	AF
727	V2-13	lambda	98	2	AF
728	V2-13	lambda	98	2	AF
729	V2-13	lambda	98	2	AF
730	V2-13	lambda	98	2	AF
731	V2-13	lambda	96	2	AF
732	V2-13	lambda	97	2	AF
733	V2-13	lambda	98	2	AF
734	V2-13	lambda	97	2	AF
735	V2-13	lambda	98	2	AF
736	V2-13	lambda	98	2	AF
737	V2-13	lambda	98	2	AF
738	V2-13	lambda	98	2	AF
739	V2-13	lambda	98	2	AF
740	V2-13	lambda	98	2	AF
741	V2-13	lambda	98	2	AF
742	V2-13	lambda	98	2	AF
743	V2-13	lambda	98	2	AF
744	V2-13	lambda	98	2	AF
745	V2-13	lambda	98	2	AF
746	V2-13	lambda	98	2	AF
747	V2-13	lambda	96	2	AF
748	V2-13	lambda	96	2	AF
749	V2-13	lambda	97	2	AF
750	V2-13	lambda	98	2	AF
751	V2-13	lambda	98	2	AF
752	V2-13	lambda	97	2	AF
753	V2-13	lambda	98	2	AF
754	V2-13	lambda	98	2	AF
755	V2-13	lambda	98	2	AF
756	V2-13	lambda	97	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
757	V2-13	lambda	97	2	AF
758	V2-13	lambda	98	2	AF
759	V2-13	lambda	98	2	AF
760	V2-13	lambda	98	2	AF
761	V2-13	lambda	96	2	AF
762	V2-13	lambda	98	2	AF
763	V2-13	lambda	97	2	AF
764	V2-13	lambda	98	2	AF
765	V2-13	lambda	98	2	AF
766	V2-13	lambda	96	2	AF
767	V2-13	lambda	98	2	AF
768	V2-13	lambda	98	2	AF
769	V2-13	lambda	98	2	AF
770	V2-13	lambda	98	2	AF
771	V2-13	lambda	98	2	AF
772	V2-13	lambda	97	2	AF
773	V2-13	lambda	98	2	AF
774	V2-13	lambda	98	2	AF
775	V2-13	lambda	97	2	AF
776	V2-13	lambda	98	2	AF
777	V2-13	lambda	91	2	AF
778	V2-13	lambda	95	2	AF
779	V2-13	lambda	98	2	AF
780	V2-13	lambda	98	2	AF
781	V2-13	lambda	98	2	AF
782	V2-13	lambda	97	2	AF
783	V2-13	lambda	98	2	AF
784	V2-13	lambda	98	2	AF
785	V2-13	lambda	98	2	AF
786	V2-13	lambda	96	2	AF
787	V2-13	lambda	95	2	AF
788	V2-13	lambda	97	2	AF
789	V2-13	lambda	97	2	AF
790	V2-13	lambda	95	2	AF
791	V2-13	lambda	95	2	AF
792	V2-13	lambda	97	2	AF
793	V2-13	lambda	96	2	AF
794	V2-13	lambda	97	2	AF
795	V2-13	lambda	97	2	AF
796	V2-13	lambda	97	2	AF
797	V2-13	lambda	95	2	AF
798	V2-13	lambda	97	2	AF

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
799	V2-13	lambda	97	2	AF
800	V2-13	lambda	98	2	AF
801	V2-13	lambda	97	2	AF
802	V2-13	lambda	98	2	AF
803	V2-13	lambda	97	2	AF
804	V2-13	lambda	98	2	AF
805	V2-13	lambda	98	2	AF
806	V2-13	lambda	98	2	AF
807	V2-13	lambda	95	2	AF
808	V2-13	lambda	97	2	AF
809	V2-13	lambda	97	2	AF
810	V2-13	lambda	97	2	AF
811	V2-13	lambda	97	2	AF
812	V2-13	lambda	98	2	AF
813	V2-13	lambda	96	2	AF
814	V2-13	lambda	98	2	AF
815	V2-13	lambda	98	2	AF
816	V2-13	lambda	96	2	AF
817	V2-13	lambda	96	2	AF
818	V2-13	lambda	98	2	AF
819	V2-13	lambda	96	2	AF
820	V2-13	lambda	98	2	AF
821	V2-13	lambda	98	2	AF
822	V2-13	lambda	96	2	AF
823	V2-13	lambda	98	2	AF
824	V2-13	lambda	98	2	AF
825	V2-13	lambda	97	2	AF
826	V2-13	lambda	96	2	AF
827	V2-13	lambda	95	2	AF
828	V2-13	lambda	98	2	AF
829	V2-13	lambda	97	2	AF
830	V2-13	lambda	98	2	AF
831	V2-13	lambda	97	2	AF
832	V2-13	lambda	95	2	AF
833	V2-13	lambda	98	2	AF
834	V2-13	lambda	90	-1	
835	V2-13	lambda	97	-1	
836	V1-4	lambda	94	0	
837	V1-4	lambda	94	0	
838	V1-3	lambda	85	0	
839	V1-4	lambda	94	0	
840	V1-4	lambda	94	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
841	V1-4	lambda	94	0	
842	V2-13	lambda	91	-1	
843	V1-4	lambda	94	0	
844	V2-13	lambda	92	2	AL
845	V1-4	lambda	95	0	
846	V1-4	lambda	94	0	
847	V1-4	lambda	94	0	
848	V2-13	lambda	90	-1	
849	V1-4	lambda	94	0	
850	V2-13	lambda	90	-1	
851	V2-13	lambda	90	-1	
852	V1-4	lambda	94	0	
853	V1-4	lambda	94	0	
854	V1-4	lambda	94	0	
855	V1-4	lambda	94	0	
856	V2-13	lambda	93	2	AL
857	V1-19	lambda	94	1	A
858	V1-16	lambda	85	0	
859	V1-3	lambda	94	0	
860	V1-16	lambda	90	0	
861	V1-19	lambda	95	1	A
862	V1-2	lambda	84	1	A
863	V1-16	lambda	91	2	AL
864	V1-16	lambda	93	1	A
865	V1-19	lambda	95	1	A
866	V1-16	lambda	89	2	AL
867	V1-4	lambda	94	0	
868	V1-4	lambda	93	0	
869	V1-13	lambda	89	1	A
870	V1-3	lambda	85	0	
871	V1-16	lambda	90	0	
872	V1-4	lambda	94	0	
873	V1-4	lambda	94	0	
874	V1-4	lambda	93	0	
875	V1-4	lambda	94	0	
876	V1-4	lambda	94	0	
877	V2-13	lambda	95	-1	
878	V1-16	lambda	89	0	
879	V1-4	lambda	94	0	
880	V1-4	lambda	94	0	
881	V1-4	lambda	94	0	
882	V1-4	lambda	94	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
883	V1-4	lambda	94	0	
884	V1-4	lambda	94	0	
885	V1-4	lambda	93	0	
886	V1-4	lambda	94	0	
887	V1-4	lambda	94	0	
888	V1-4	lambda	90	0	
889	V1-4	lambda	94	0	
890	V3-4	lambda	88	1	A
891	V3-4	lambda	88	1	A
892	V2-13	lambda	91	-1	
893	V2-13	lambda	98	-1	
894	V3-4	lambda	88	1	A
895	V2-13	lambda	89	2	AL
896	V2-13	lambda	92	-1	
897	V1-17	lambda	91	2	AL
898	V1-16	lambda	91	1	A
899	V2-1	lambda	88	1	A
900	V2-13	lambda	98	-1	
901	V1-16	lambda	91	1	A
902	V1-16	lambda	87	1	A
903	V3-4	lambda	88	1	A
904	V1-13	lambda	97	1	A
905	A27	kappa	90	2	AL
906	V1-4	lambda	86	1	A
907	V1-4	lambda	88	1	A
908	V2-13	lambda	90	-1	
909	V1-22	lambda	93	2	AL
910	V3-4	lambda	88	1	A
911	V2-13	lambda	91	-1	
912	V2-13	lambda	97	-1	
913	V2-13	lambda	98	-1	
914	V2-13	lambda	97	-1	
915	V1-4	lambda	94	0	
916	V2-13	lambda	97	-1	
917	V1-4	lambda	89	0	
918	L12	kappa	88	0	
919	L1	kappa	87	0	
920	V2-13	lambda	98	-1	
921	V2-13	lambda	93	2	AL
922	L12	kappa	88	0	
923	V1-4	lambda	94	0	
924	V2-13	lambda	97	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
925	V1-4	lambda	89	0	
926	L12	kappa	88	0	
927	V2-13	lambda	97	-1	
928	V2-13	lambda	100	-1	
929	V1-19	lambda	83	0	
930	V1-4	lambda	93	0	
931	V1-4	lambda	94	0	
932	L12	kappa	88	0	
933	V1-4	lambda	93	0	
934	V1-16	lambda	85	0	
935	V1-19	lambda	83	0	
936	L8	kappa	89	0	
937	V2-13	lambda	98	-1	
938	V2-13	lambda	98	-1	
939	V1-19	lambda	83	0	
940	V1-4	lambda	93	0	
941	V1-4	lambda	94	0	
942	V1-4	lambda	93	0	
943	V2-13	lambda	98	-1	
944	V1-4	lambda	94	0	
945	V1-4	lambda	93	0	
946	V2-13	lambda	90	-1	
947	V1-4	lambda	94	0	
948	V2-13	lambda	96	-1	
949	V2-13	lambda	97	-1	
950	V2-13	lambda	91	-1	
951	V1-4	lambda	93	0	
952	V2-13	lambda	98	-1	
953	V2-13	lambda	94	-1	
954	V1-4	lambda	93	0	
955	V1-4	lambda	94	0	
956	V1-4	lambda	93	0	
957	V2-13	lambda	90	-1	
958	V1-4	lambda	94	0	
959	V2-13	lambda	89	-1	
960	V1-4	lambda	94	0	
961	V1-4	lambda	94	0	
962	V1-4	lambda	94	0	
963	V2-13	lambda	98	-1	
964	V1-4	lambda	94	0	
965	V2-13	lambda	92	-1	
966	V1-4	lambda	94	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
967	V2-13	lambda	98	-1	
968	V1-4	lambda	93	0	
969	L12	kappa	88	0	
970	V2-13	lambda	98	-1	
971	V1-4	lambda	94	0	
972	V1-4	lambda	94	0	
973	V1-19	lambda	83	0	
974	V2-13	lambda	90	-1	
975	V1-4	lambda	94	0	
976	V1-4	lambda	94	0	
977	V1-4	lambda	93	0	
978	V1-4	lambda	94	0	
979	V1-4	lambda	93	0	
980	V2-13	lambda	95	-1	
981	V1-4	lambda	94	0	
982	V2-13	lambda	98	-1	
983	V1-4	lambda	94	0	
984	V2-13	lambda	97	-1	
985	V1-4	lambda	94	0	
986	V1-4	lambda	93	0	
987	V2-13	lambda	97	-1	
988	V1-19	lambda	84	0	
989	V1-4	lambda	94	0	
990	V1-4	lambda	94	0	
991	V1-4	lambda	94	0	
992	V1-4	lambda	94	0	
993	V2-13	lambda	90	-1	
994	V1-4	lambda	94	0	
995	V1-4	lambda	94	0	
996	V2-13	lambda	98	-1	
997	V2-13	lambda	97	-1	
998	V1-4	lambda	94	0	
999	V2-13	lambda	89	-1	
1000	V1-4	lambda	94	0	
1001	V1-4	lambda	94	0	
1002	V1-4	lambda	94	0	
1003	V1-4	lambda	94	0	
1004	O12	kappa	89	0	
1005	V1-4	lambda	94	0	
1006	V1-4	lambda	94	0	
1007	V1-4	lambda	92	0	
1008	L12	kappa	87	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1009	V1-17	lambda	92	1	A
1010	V1-4	lambda	92	1	A
1011	V1-16	lambda	95	1	A
1012	V1-13	lambda	93	1	A
1013	V1-4	lambda	92	1	A
1014	V2-13	lambda	86	2	AL
1015	V1-19	lambda	94	1	A
1016	V1-17	lambda	91	2	AL
1017	V1-16	lambda	92	1	A
1018	V2-1	lambda	90	1	A
1019	V2-14	lambda	87	1	A
1020	V1-16	lambda	92	2	AL
1021	V1-17	lambda	92	2	AL
1022	V2-13	lambda	90	2	AL
1023	V1-13	lambda	87	1	A
1024	V2-14	lambda	87	1	A
1025	V1-16	lambda	92	1	A
1026	V2-13	lambda	86	2	AL
1027	O12	kappa	88	2	AL
1028	V2-13	lambda	98	2	AL
1029	V1-19	lambda	87	1	A
1030	V1-17	lambda	82	2	AL
1031	V1-13	lambda	88	1	A
1032	V1-13	lambda	86	1	A
1033	V1-13	lambda	88	1	A
1034	V1-13	lambda	91	1	A
1035	A27	kappa	91	2	AL
1036	V1-13	lambda	88	1	A
1037	V1-17	lambda	93	1	A
1038	V1-16	lambda	90	1	A
1039	A19	kappa	91	2	AL
1040	V1-16	lambda	86	1	A
1041	V1-13	lambda	86	1	A
1042	V1-17	lambda	88	1	A
1043	V1-13	lambda	85	1	A
1044	V1-4	lambda	93	0	
1045	V1-13	lambda	94	1	A
1046	V1-4	lambda	94	0	
1047	V1-4	lambda	94	0	
1048	V1-16	lambda	94	2	AL
1049	L6	kappa	100	2	AL
1050	V2-13	lambda	93	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1051	V1-4	lambda	92	0	
1052	V1-4	lambda	94	0	
1053	V1-4	lambda	94	0	
1054	V2-13	lambda	98	-1	
1055	V1-4	lambda	94	0	
1056	V2-13	lambda	96	-1	
1057	V1-4	lambda	94	0	
1058	V1-4	lambda	93	0	
1059	V1-4	lambda	94	0	
1060	V1-4	lambda	94	0	
1061	V1-4	lambda	94	0	
1062	V1-4	lambda	93	0	
1063	V1-4	lambda	93	0	
1064	V1-4	lambda	93	0	
1065	V2-13	lambda	98	-1	
1066	V1-4	lambda	94	0	
1067	V1-4	lambda	94	0	
1068	V1-4	lambda	94	0	
1069	V1-4	lambda	92	0	
1070	V1-4	lambda	94	0	
1071	V1-4	lambda	93	0	
1072	V1-4	lambda	94	0	
1073	V1-4	lambda	94	0	
1074	V1-4	lambda	94	0	
1075	V1-4	lambda	93	0	
1076	V1-4	lambda	93	0	
1077	V1-4	lambda	94	0	
1078	V1-4	lambda	94	0	
1079	V1-4	lambda	94	0	
1080	V1-4	lambda	94	0	
1081	V1-4	lambda	94	0	
1082	V1-4	lambda	94	0	
1083	V1-4	lambda	93	0	
1084	V1-4	lambda	94	0	
1085	V1-4	lambda	94	0	
1086	V1-4	lambda	94	0	
1087	V1-4	lambda	93	0	
1088	V1-4	lambda	94	0	
1089	V1-4	lambda	94	0	
1090	V1-16	lambda	89	0	
1091	V1-4	lambda	93	0	
1092	V1-4	lambda	94	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1093	V1-4	lambda	94	0	
1094	V1-4	lambda	94	0	
1095	V1-4	lambda	93	0	
1096	V1-4	lambda	94	0	
1097	V1-4	lambda	94	0	
1098	V1-4	lambda	93	0	
1099	V1-16	lambda	87	0	
1100	V1-4	lambda	94	0	
1101	V1-4	lambda	94	0	
1102	V2-13	lambda	90	-1	
1103	V1-4	lambda	94	0	
1104	L19	kappa	82	0	
1105	V2-13	lambda	91	-1	
1106	V1-4	lambda	94	0	
1107	V1-4	lambda	94	0	
1108	V2-13	lambda	91	-1	
1109	V2-13	lambda	98	-1	
1110	V2-13	lambda	91	-1	
1111	V2-13	lambda	91	-1	
1112	V2-13	lambda	96	-1	
1113	V2-13	lambda	91	-1	
1114	V1-4	lambda	94	0	
1115	V2-13	lambda	89	-1	
1116	V2-13	lambda	89	-1	
1117	V2-13	lambda	91	-1	
1118	V2-13	lambda	91	-1	
1119	V2-13	lambda	91	-1	
1120	V2-13	lambda	91	-1	
1121	V3-4	lambda	88	1	A
1122	V1-11	lambda	94	1	A
1123	V2-14	lambda	92	1	A
1124	V1-16	lambda	95	1	A
1125	V1-22	lambda	93	2	AL
1126	V3-4	lambda	88	1	A
1127	V3-4	lambda	88	1	A
1128	V1-16	lambda	93	2	AL
1129	V1-16	lambda	90	0	
1130	V1-16	lambda	90	1	A
1131	V1-17	lambda	91	2	AL
1132	V1-4	lambda	93	0	
1133	V1-13	lambda	93	1	A
1134	V1-16	lambda	95	1	A

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1135	V1-17	lambda	91	2	AL
1136	V1-13	lambda	86	1	A
1137	V1-16	lambda	86	1	A
1138	V2-13	lambda	84	2	AL
1139	V1-19	lambda	92	1	A
1140	V3-4	lambda	88	1	A
1141	V3-4	lambda	88	1	A
1142	V1-13	lambda	91	1	A
1143	V1-4	lambda	94	0	
1144	V1-13	lambda	96	1	A
1145	V1-17	lambda	90	2	AL
1146	V1-19	lambda	89	1	A
1147	V3-4	lambda	87	1	A
1148	V3-4	lambda	88	1	A
1149	V3-4	lambda	82	1	A
1150	V4-2	lambda	82	1	A
1151	V3-4	lambda	86	1	A
1152	V3-4	lambda	86	1	A
1153	V1-13	lambda	94	1	A
1154	V1-13	lambda	90	1	A
1155	V1-16	lambda	85	1	A
1156	V1-19	lambda	96	1	A
1157	V3-4	lambda	88	1	A
1158	V1-16	lambda	91	1	A
1159	V3-4	lambda	76	1	A
1160	V3-4	lambda	83	1	A
1161	V2-14	lambda	92	1	A
1162	V3-4	lambda	88	1	A
1163	V1-17	lambda	91	2	AL
1164	V1-13	lambda	78	1	A
1165	V1-13	lambda	86	1	A
1166	V3-4	lambda	87	1	A
1167	V1-22	lambda	94	2	AL
1168	V2-13	lambda	83	2	AL
1169	V1-19	lambda	84	1	A
1170	V2-13	lambda	90	-1	
1171	V1-3	lambda	85	0	
1172	V1-4	lambda	94	0	
1173	V1-4	lambda	89	0	
1174	O12	kappa	94	0	
1175	V1-4	lambda	93	0	
1176	V1-4	lambda	93	0	

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after (Gly4Ser)3 sequence prior to amino acid position no 1 in VL region	Identity of amino acids after (Gly4Ser)3 sequence prior to amino acid position no. 1 in VL region
1177	L12	kappa	88	0	
1178	V2-13	lambda	89	-1	
1179	V2-13	lambda	90	-1	
1180	V1-4	lambda	94	0	
1181	V2-13	lambda	91	-1	
1182	V2-13	lambda	91	-1	
1183	V1-19	lambda	83	0	
1184	V1-4	lambda	94	0	
1185	V1-4	lambda	94	0	
1186	V1-4	lambda	92	0	
1187	V1-4	lambda	94	0	
1188	L12	kappa	88	0	
1189	V2-13	lambda	97	-1	
1190	V1-4	lambda	93	0	
1191	V1-4	lambda	94	0	
1192	V2-13	lambda	97	-1	
1193	V1-16	lambda	90	0	
1194	V1-4	lambda	94	0	
1195	V1-4	lambda	94	0	
1196	V1-4	lambda	94	0	
1197	V1-4	lambda	94	0	
1198	V2-13	lambda	90	-1	
1199	V1-16	lambda	88	1	A
1200	V1-19	lambda	86	1	A
1201	V1-13	lambda	90	1	A
1202	V1-17	lambda	92	1	A
1203	V1-16	lambda	97	1	A
1204	V2-13	lambda	93	2	AL
1205	V2-13	lambda	93	2	AL
1206	V2-1	lambda	86	1	A
1207	V2-13	lambda	84	2	AL
1208	V1-13	lambda	94	1	A
1209	V1-4	lambda	89	1	A
1210	V1-16	lambda	98	1	A
1211	V1-16	lambda	100	1	A
1212	V1-17	lambda	95	1	A
1213	V1-13	lambda	97	1	A
1214	V1-16	lambda	100	1	A
1215	V2-13	lambda	83	2	AL
1216	V1-16	lambda	83	1	A
1217	V1-13	lambda	87	1	A
1218	V1-17	lambda	89	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1219	A27	kappa	97	2	AL
1220	V1-17	lambda	86	1	A
1221	V1-13	lambda	93	1	A
1222	V1-17	lambda	86	1	A
1223	V1-16	lambda	95	1	A
1224	V1-17	lambda	86	1	A
1225	V1-13	lambda	95	1	A
1226	V1-13	lambda	82	1	A
1227	V1-16	lambda	94	2	AL
1228	V1-16	lambda	98	1	A
1229	V1-16	lambda	94	1	A
1230	V4-2	lambda	95	1	A
1231	V1-13	lambda	90	1	A
1232	V2-13	lambda	89	2	AL
1233	V1-2	lambda	92	1	A
1234	V1-22	lambda	93	2	AL
1235	V1-13	lambda	98	1	A
1236	V1-17	lambda	91	2	AL
1237	V1-13	lambda	88	1	A
1238	L16	kappa	91	2	AL
1239	V1-19	lambda	89	1	A
1240	V1-17	lambda	92	1	A
1241	V1-4	lambda	82	1	A
1242	V1-19	lambda	84	1	A
1243	V1-16	lambda	86	1	A
1244	V1-16	lambda	95	2	AL
1245	V1-20	lambda	83	1	A
1246	V1-19	lambda	96	1	A
1247	V1-2	lambda	89	1	A
1248	V1-17	lambda	91	1	A
1249	V1-2	lambda	90	1	A
1250	V1-16	lambda	91	2	AL
1251	V2-13	lambda	94	2	AL
1252	V2-13	lambda	93	2	AL
1253	V1-16	lambda	94	1	A
1254	V1-17	lambda	92	1	A
1255	V1-17	lambda	96	1	A
1256	V1-13	lambda	78	1	A
1257	V2-13	lambda	95	2	AL
1258	V2-13	lambda	89	2	AL
1259	V2-13	lambda	93	2	AL
1260	V1-19	lambda	98	1	A

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1261	V2-13	lambda	86	2	AL
1262	V1-16	lambda	93	1	A
1263	V1-13	lambda	92	1	A
1264	A27	kappa	100	2	AL
1265	V1-16	lambda	98	1	A
1266	V1-16	lambda	91	1	A
1267	V1-17	lambda	92	1	A
1268	L16	kappa	96	2	AL
1269	V1-16	lambda	93	2	AL
1270	V1-13	lambda	85	1	A
1271	V1-11	lambda	76	1	A
1272	V1-16	lambda	94	1	A
1273	V1-17	lambda	90	1	A
1274	V1-16	lambda	89	1	A
1275	V1-13	lambda	95	1	A
1276	V1-19	lambda	92	1	A
1277	V1-16	lambda	92	2	AL
1278	V4-2	lambda	82	1	A
1279	V1-16	lambda	88	1	A
1280	V1-13	lambda	95	1	A
1281	V1-13	lambda	86	1	A
1282	V1-13	lambda	95	1	A
1283	V1-17	lambda	94	1	A
1284	V1-17	lambda	90	1	A
1285	V1-13	lambda	82	1	A
1286	V1-16	lambda	90	1	A
1287	V1-3	lambda	85	0	
1288	V1-3	lambda	85	0	
1289	V1-4	lambda	94	0	
1290	V2-13	lambda	90	-1	
1291	O12	kappa	89	0	
1292	V1-4	lambda	93	0	
1293	V2-13	lambda	98	-1	
1294	V2-13	lambda	96	-1	
1295	V1-3	lambda	85	0	
1296	V1-16	lambda	89	0	
1297	V1-4	lambda	94	0	
1298	V1-16	lambda	90	0	
1299	V2-13	lambda	89	-1	
1300	V2-13	lambda	97	-1	
1301	V1-19	lambda	83	0	
1302	V1-4	lambda	93	0	

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SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1303	V2-13	lambda	98	-1	
1304	V1-4	lambda	94	0	
1305	V2-13	lambda	98	-1	
1306	V2-13	lambda	92	-1	
1307	V2-13	lambda	95	-1	
1308	V2-13	lambda	97	-1	
1309	V1-19	lambda	83	0	
1310	L8	kappa	88	0	
1311	V1-4	lambda	94	0	
1312	V2-13	lambda	93	0	
1313	V1-4	lambda	94	0	
1314	V1-4	lambda	94	0	
1315	V2-13	lambda	98	-1	
1316	V2-13	lambda	97	-1	
1317	V1-4	lambda	93	0	
1318	V1-4	lambda	93	0	
1319	V1-4	lambda	92	0	
1320	L12	kappa	88	0	
1321	O12	kappa	89	0	
1322	V2-13	lambda	98	-1	
1323	V2-13	lambda	97	-1	
1324	V1-4	lambda	93	0	
1325	V1-4	lambda	94	0	
1326	V1-4	lambda	94	0	
1327	V1-4	lambda	94	0	
1328	V2-13	lambda	97	-1	
1329	V1-4	lambda	93	0	
1330	V2-13	lambda	90	-1	
1331	V2-13	lambda	98	-1	
1332	V1-4	lambda	94	0	
1333	V1-4	lambda	94	0	
1334	V1-4	lambda	94	0	
1335	V2-13	lambda	98	-1	
1336	V1-4	lambda	94	0	
1337	V1-4	lambda	94	0	
1338	V1-4	lambda	94	0	
1339	V1-4	lambda	94	0	
1340	V1-4	lambda	94	0	
1341	V2-13	lambda	91	-1	
1342	V1-4	lambda	94	0	
1343	V1-4	lambda	68	0	
1344	V2-13	lambda	90	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1345	V1-4	lambda	94	0	
1346	V2-13	lambda	98	-1	
1347	V1-16	lambda	89	0	
1348	V1-16	lambda	90	0	
1349	V1-16	lambda	90	0	
1350	V1-4	lambda	94	0	
1351	V1-4	lambda	93	0	
1352	V1-4	lambda	93	0	
1353	V1-4	lambda	93	0	
1354	V1-4	lambda	94	0	
1355	V1-4	lambda	94	0	
1356	V1-4	lambda	93	0	
1357	V2-13	lambda	97	-1	
1358	V1-13	lambda	92	1	A
1359	V1-13	lambda	96	1	A
1360	O12	kappa	85	2	AL
1361	V1-2	lambda	85	1	A
1362	V1-13	lambda	89	1	A
1363	V1-16	lambda	87	1	A
1364	V1-2	lambda	92	1	A
1365	V1-4	lambda	90	1	A
1366	V1-16	lambda	86	1	A
1367	V2-13	lambda	90	-1	
1368	V1-16	lambda	96	1	A
1369	V1-16	lambda	100	1	A
1370	V2-13	lambda	90	-1	
1371	V1-4	lambda	91	1	A
1372	V1-4	lambda	90	1	A
1373	V3-4	lambda	88	1	A
1374	V2-13	lambda	95	2	AL
1375	V1-22	lambda	92	2	AL
1376	V1-20	lambda	90	2	AL
1377	V2-14	lambda	92	1	A
1378	V1-13	lambda	90	1	A
1379	V1-4	lambda	93	0	
1380	V1-4	lambda	94	0	
1381	V1-4	lambda	91	0	
1382	V1-4	lambda	94	0	
1383	V1-4	lambda	93	0	
1384	V2-13	lambda	97	-1	
1385	O12	kappa	89	0	
1386	V2-13	lambda	98	-1	

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SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1387	V2-13	lambda	90	-1	
1388	V2-13	lambda	97	-1	
1389	V1-16	lambda	85	-1	
1390	V1-4	lambda	94	0	
1391	V2-13	lambda	98	-1	
1392	V1-4	lambda	94	0	
1393	V2-13	lambda	89	-1	
1394	V2-13	lambda	89	-1	
1395	V1-4	lambda	92	0	
1396	V1-4	lambda	94	0	
1397	V1-4	lambda	94	0	
1398	V1-4	lambda	93	0	
1399	V1-4	lambda	94	0	
1400	V1-16	lambda	90	0	
1401	V1-4	lambda	94	0	
1402	V2-13	lambda	90	-1	
1403	V1-4	lambda	94	0	
1404	V1-4	lambda	93	0	
1405	V1-4	lambda	94	0	
1406	V1-4	lambda	94	0	
1407	V1-4	lambda	94	0	
1408	V1-4	lambda	94	0	
1409	V1-4	lambda	93	0	
1410	O12	kappa	89	0	
1411	V1-16	lambda	84	0	
1412	V1-4	lambda	93	0	
1413	V1-4	lambda	89	0	
1414	V1-16	lambda	90	0	
1415	V1-4	lambda	94	0	
1416	V2-13	lambda	97	-1	
1417	V2-13	lambda	97	-1	
1418	V1-4	lambda	94	0	
1419	V1-19	lambda	83	0	
1420	V1-16	lambda	90	0	
1421	L12	kappa	87	0	
1422	V1-16	lambda	90	0	
1423	V1-4	lambda	94	0	
1424	V2-13	lambda	97	-1	
1425	V2-13	lambda	98	-1	
1426	V2-13	lambda	98	-1	
1427	V1-4	lambda	93	0	
1428	V1-4	lambda	94	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1429	V1-16	lambda	90	0	
1430	V1-16	lambda	90	0	
1431	V1-4	lambda	94	0	
1432	V1-4	lambda	94	0	
1433	V2-13	lambda	96	-1	
1434	V1-4	lambda	94	0	
1435	V1-4	lambda	94	0	
1436	V1-16	lambda	90	0	
1437	V1-4	lambda	93	0	
1438	V2-13	lambda	90	-1	
1439	V1-4	lambda	94	0	
1440	V1-4	lambda	94	0	
1441	V1-4	lambda	94	0	
1442	V1-4	lambda	93	0	
1443	V1-19	lambda	83	0	
1444	V2-13	lambda	98	-1	
1445	V2-13	lambda	98	-1	
1446	L11	kappa	92	0	
1447	V1-19	lambda	83	0	
1448	V1-16	lambda	85	0	
1449	V1-4	lambda	94	0	
1450	V1-4	lambda	94	0	
1451	V1-4	lambda	94	0	
1452	V1-4	lambda	94	0	
1453	V1-4	lambda	94	0	
1454	V1-4	lambda	93	0	
1455	V1-16	lambda	90	0	
1456	V2-13	lambda	91	2	AL
1457	V1-16	lambda	88	0	
1458	V1-16	lambda	90	0	
1459	V1-4	lambda	94	0	
1460	V1-4	lambda	94	0	
1461	V1-16	lambda	90	0	
1462	V1-2	lambda	84	0	
1463	V1-16	lambda	90	0	
1464	V1-16	lambda	90	0	
1465	V1-19	lambda	93	1	A
1466	V1-16	lambda	79	1	A
1467	V1-4	lambda	82	1	A
1468	V2-13	lambda	97	2	AL
1469	V1-17	lambda	94	1	A
1470	V2-13	lambda	95	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1471	V1-4	lambda	93	0	
1472	V2-13	lambda	95	-1	
1473	V1-4	lambda	92	0	
1474	V2-13	lambda	97	-1	
1475	V2-13	lambda	89	2	AL
1476	V1-4	lambda	94	0	
1477	V1-16	lambda	90	0	
1478	V1-4	lambda	94	0	
1479	V1-4	lambda	94	0	
1480	V2-1	lambda	90	1	A
1481	V1-16	lambda	93	1	A
1482	V2-13	lambda	87	2	AL
1483	V2-13	lambda	92	2	AL
1484	V2-13	lambda	86	2	AL
1485	V4-2	lambda	85	1	A
1486	V2-13	lambda	89	2	AL
1487	V1-13	lambda	94	1	A
1488	V2-1	lambda	87	2	AL
1489	V1-13	lambda	94	1	A
1490	V2-13	lambda	90	2	AL
1491	V1-17	lambda	95	1	A
1492	V1-13	lambda	89	1	A
1493	V1-16	lambda	89	1	A
1494	V1-13	lambda	90	1	A
1495	V1-13	lambda	86	1	A
1496	V1-2	lambda	89	1	A
1497	V1-13	lambda	99	1	A
1498	V1-19	lambda	88	1	A
1499	A27	kappa	95	2	AL
1500	V1-16	lambda	97	1	A
1501	V1-19	lambda	84	1	A
1502	V2-1	lambda	89	2	AL
1503	V1-16	lambda	91	2	AL
1504	V1-13	lambda	90	1	A
1505	V1-13	lambda	89	1	A
1506	V1-13	lambda	89	1	A
1507	V1-16	lambda	98	1	A
1508	V1-13	lambda	96	1	A
1509	V2-13	lambda	100	2	AL
1510	V1-16	lambda	91	1	A
1511	V2-13	lambda	93	2	AL
1512	V1-16	lambda	89	1	A

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1513	V1-17	lambda	86	1	A
1514	V1-17	lambda	91	2	AL
1515	V2-14	lambda	88	2	AL
1516	V1-13	lambda	91	1	A
1517	V1-16	lambda	95	1	A
1518	V1-16	lambda	91	1	A
1519	V1-13	lambda	92	1	A
1520	V1-2	lambda	93	1	A
1521	V1-13	lambda	92	1	A
1522	V1-19	lambda	86	1	A
1523	V3-2	lambda	93	1	A
1524	V1-16	lambda	96	1	A
1525	V1-4	lambda	93	1	A
1526	V2-13	lambda	96	2	AL
1527	V1-16	lambda	97	2	AL
1528	V1-16	lambda	88	1	A
1529	V1-17	lambda	90	1	A
1530	V2-13	lambda	90	2	AL
1531	V1-22	lambda	88	2	AL
1532	V1-13	lambda	79	1	A
1533	V2-7	lambda	84	2	AL
1534	A27	kappa	94	2	AL
1535	V2-13	lambda	94	2	AL
1536	V1-16	lambda	92	1	A
1537	V1-16	lambda	87	1	A
1538	V1-19	lambda	92	1	A
1539	V1-13	lambda	93	1	A
1540	V2-14	lambda	76	2	AL
1541	V2-13	lambda	90	2	AL
1542	V1-16	lambda	96	1	A
1543	V1-13	lambda	83	1	A
1544	V1-2	lambda	93	1	A
1545	V1-19	lambda	82	1	A
1546	V1-16	lambda	93	1	A
1547	V1-16	lambda	86	2	AL
1548	V2-13	lambda	97	2	AL
1549	V1-19	lambda	91	1	A
1550	V1-17	lambda	88	1	A
1551	V1-19	lambda	93	1	A
1552	V4-2	lambda	85	1	A
1553	V1-16	lambda	91	1	A
1554	V1-16	lambda	87	1	A

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1555	V2-13	lambda	86	2	AL
1556	V1-19	lambda	91	1	A
1557	V1-13	lambda	92	1	A
1558	V1-2	lambda	85	1	A
1559	V1-2	lambda	76	1	A
1560	V1-4	lambda	92	0	
1561	V1-4	lambda	93	0	
1562	V1-4	lambda	93	0	
1563	V2-14	lambda	83	1	A
1564	V2-14	lambda	83	1	A
1565	V1-19	lambda	94	1	A
1566	V1-19	lambda	94	1	A
1567	V1-19	lambda	83	0	
1568	V1-13	lambda	93	1	A
1569	V1-16	lambda	88	1	A
1570	V2-14	lambda	83	1	A
1571	V1-19	lambda	93	1	A
1572	V1-19	lambda	94	1	A
1573	V1-19	lambda	94	1	A
1574	V2-14	lambda	83	1	A
1575	V1-13	lambda	91	1	A
1576	V1-4	lambda	94	0	
1577	L11	kappa	91	0	
1578	V1-4	lambda	94	0	
1579	V1-4	lambda	93	0	
1580	O12	kappa	89	0	
1581	V1-4	lambda	94	0	
1582	V1-17	lambda	94	1	A
1583	V1-16	lambda	80	1	A
1584	V1-13	lambda	98	1	A
1585	V1-13	lambda	89	1	A
1586	V1-4	lambda	94	0	
1587	V1-4	lambda	94	0	
1588	V2-13	lambda	91	-1	
1589	V1-4	lambda	94	0	
1590	V1-16	lambda	93	2	AL
1591	V1-16	lambda	91	1	A
1592	V2-13	lambda	84	2	AL
1593	V1-4	lambda	94	0	
1594	V2-13	lambda	90	-1	
1595	V1-4	lambda	94	0	
1596	V2-13	lambda	98	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1597	V1-16	lambda	90	0	
1598	V1-16	lambda	90	0	
1599	V1-3	lambda	85	0	
1600	V1-16	lambda	90	0	
1601	V1-4	lambda	93	0	
1602	V1-4	lambda	93	0	
1603	L12	kappa	88	0	
1604	V1-4	lambda	93	0	
1605	V1-4	lambda	94	0	
1606	V1-4	lambda	94	0	
1607	V1-19	lambda	83	0	
1608	V1-4	lambda	93	0	
1609	V2-13	lambda	98	-1	
1610	V1-19	lambda	82	0	
1611	V1-19	lambda	82	0	
1612	V1-4	lambda	94	0	
1613	V1-4	lambda	94	0	
1614	V1-16	lambda	90	0	
1615	V2-13	lambda	98	-1	
1616	V1-4	lambda	94	0	
1617	V1-4	lambda	93	0	
1618	V1-19	lambda	83	0	
1619	V1-4	lambda	94	0	
1620	V2-13	lambda	98	-1	
1621	V2-13	lambda	98	-1	
1622	V2-13	lambda	98	-1	
1623	V2-13	lambda	98	-1	
1624	V2-13	lambda	98	-1	
1625	V1-4	lambda	94	0	
1626	V1-4	lambda	91	0	
1627	V1-4	lambda	94	0	
1628	V2-13	lambda	97	-1	
1629	V1-4	lambda	93	0	
1630	V1-16	lambda	90	0	
1631	V1-19	lambda	84	0	
1632	V1-7	lambda	93	0	
1633	V1-4	lambda	94	0	
1634	V1-4	lambda	94	0	
1635	A20	kappa	90	0	
1636	V1-4	lambda	94	0	
1637	V1-4	lambda	93	0	
1638	V2-13	lambda	89	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1639	V2-13	lambda	89	-1	
1640	V1-4	lambda	94	0	
1641	V2-13	lambda	98	-1	
1642	V1-16	lambda	90	0	
1643	V2-13	lambda	98	-1	
1644	V1-4	lambda	94	0	
1645	V1-4	lambda	94	0	
1646	V2-13	lambda	98	-1	
1647	V2-13	lambda	98	-1	
1648	V2-13	lambda	98	-1	
1649	V1-4	lambda	94	0	
1650	V1-4	lambda	94	0	
1651	V2-13	lambda	98	-1	
1652	V2-13	lambda	90	-1	
1653	V1-4	lambda	94	0	
1654	V1-4	lambda	94	0	
1655	V2-13	lambda	98	-1	
1656	V1-4	lambda	94	0	
1657	V2-13	lambda	96	-1	
1658	V1-4	lambda	94	0	
1659	V1-19	lambda	82	0	
1660	V2-13	lambda	97	-1	
1661	V1-4	lambda	94	0	
1662	V2-13	lambda	98	-1	
1663	V1-4	lambda	94	0	
1664	V1-4	lambda	93	0	
1665	V2-13	lambda	98	-1	
1666	V1-4	lambda	93	0	
1667	V2-13	lambda	98	-1	
1668	V2-13	lambda	98	-1	
1669	V1-4	lambda	93	0	
1670	V2-13	lambda	98	-1	
1671	V1-19	lambda	83	0	
1672	V1-4	lambda	94	0	
1673	V1-4	lambda	94	0	
1674	V1-4	lambda	94	0	
1675	V2-13	lambda	97	-1	
1676	V2-13	lambda	96	-1	
1677	V1-4	lambda	93	0	
1678	V2-13	lambda	98	-1	
1679	V2-13	lambda	98	-1	
1680	V1-4	lambda	88	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1681	V2-13	lambda	98	-1	
1682	V1-19	lambda	83	0	
1683	V1-4	lambda	94	0	
1684	V1-4	lambda	92	0	
1685	V1-4	lambda	89	0	
1686	V1-4	lambda	96	1	A
1687	V1-4	lambda	94	0	
1688	V1-4	lambda	92	0	
1689	V1-4	lambda	94	0	
1690	V1-4	lambda	93	0	
1691	V1-4	lambda	94	0	
1692	V2-13	lambda	98	-1	
1693	V1-19	lambda	83	0	
1694	V2-13	lambda	98	-1	
1695	V1-4	lambda	94	0	
1696	V1-4	lambda	94	0	
1697	V1-3	lambda	85	0	
1698	V1-19	lambda	83	0	
1699	V1-4	lambda	93	0	
1700	L12	kappa	88	0	
1701	V1-4	lambda	94	0	
1702	V2-13	lambda	96	-1	
1703	V2-13	lambda	98	-1	
1704	V1-4	lambda	93	0	
1705	V2-13	lambda	96	-1	
1706	V1-4	lambda	94	0	
1707	V1-19	lambda	83	0	
1708	V2-13	lambda	90	-1	
1709	V1-13	lambda	95	1	A
1710	V1-4	lambda	92	1	A
1711	V1-17	lambda	87	2	AL
1712	V1-13	lambda	90	1	A
1713	V1-16	lambda	85	1	A
1714	V2-17	lambda	87	2	AL
1715	V1-19	lambda	94	1	A
1716	V1-13	lambda	89	1	A
1717	O12	kappa	89	0	
1718	V2-13	lambda	97	-1	
1719	O12	kappa	89	0	
1720	V1-4	lambda	94	0	
1721	V2-13	lambda	98	-1	
1722	V2-13	lambda	98	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1723	V2-13	lambda	97	-1	
1724	V2-13	lambda	98	-1	
1725	V2-13	lambda	98	-1	
1726	V2-13	lambda	98	-1	
1727	V2-13	lambda	96	-1	
1728	V2-13	lambda	93	-1	
1729	V2-13	lambda	90	-1	
1730	V2-13	lambda	97	-1	
1731	V2-13	lambda	91	-1	
1732	V2-13	lambda	97	-1	
1733	O12	kappa	89	0	
1734	V2-13	lambda	98	-1	
1735	V1-4	lambda	94	0	
1736	V1-4	lambda	94	0	
1737	O12	kappa	89	0	
1738	V1-4	lambda	94	0	
1739	V1-4	lambda	93	0	
1740	V2-13	lambda	97	-1	
1741	V2-13	lambda	98	-1	
1742	V2-13	lambda	90	-1	
1743	V1-4	lambda	94	0	
1744	V1-4	lambda	94	0	
1745	V1-4	lambda	93	0	
1746	V1-4	lambda	94	0	
1747	V1-4	lambda	92	0	
1748	V1-4	lambda	93	0	
1749	V1-4	lambda	93	0	
1750	V1-4	lambda	93	0	
1751	V1-4	lambda	93	0	
1752	V1-4	lambda	94	0	
1753	V2-13	lambda	84	0	
1754	V1-16	lambda	89	0	
1755	V2-13	lambda	92	-1	
1756	V1-4	lambda	94	0	
1757	V1-16	lambda	90	0	
1758	V1-4	lambda	93	0	
1759	V1-4	lambda	94	0	
1760	V1-4	lambda	93	0	
1761	V2-13	lambda	90	-1	
1762	V2-13	lambda	97	-1	
1763	V1-4	lambda	94	0	
1764	V2-13	lambda	97	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1765	V2-13	lambda	91	-1	
1766	V1-16	lambda	90	0	
1767	V1-16	lambda	90	0	
1768	V1-4	lambda	94	0	
1769	V1-4	lambda	94	0	
1770	V1-4	lambda	94	0	
1771	L12	kappa	88	0	
1772	V1-4	lambda	94	0	
1773	V1-4	lambda	94	0	
1774	V1-4	lambda	94	0	
1775	V1-4	lambda	93	0	
1776	V1-4	lambda	94	0	
1777	V2-13	lambda	97	-1	
1778	L12	kappa	88	0	
1779	V1-4	lambda	92	0	
1780	V1-4	lambda	94	0	
1781	V2-13	lambda	97	-1	
1782	V1-4	lambda	94	0	
1783	V1-4	lambda	94	0	
1784	V1-4	lambda	94	0	
1785	V2-13	lambda	90	-1	
1786	V2-13	lambda	90	-1	
1787	V1-4	lambda	94	1	A
1788	V2-13	lambda	90	-1	
1789	V1-4	lambda	89	0	
1790	V2-13	lambda	97	-1	
1791	V1-4	lambda	89	0	
1792	V1-4	lambda	94	0	
1793	V1-4	lambda	92	0	
1794	V1-16	lambda	89	0	
1795	V1-4	lambda	94	0	
1796	V1-4	lambda	94	0	
1797	V1-4	lambda	94	0	
1798	V1-4	lambda	94	0	
1799	V1-4	lambda	94	0	
1800	V1-4	lambda	89	0	
1801	V1-4	lambda	94	0	
1802	V1-4	lambda	94	0	
1803	V1-4	lambda	95	0	
1804	V1-4	lambda	94	0	
1805	V1-16	lambda	81	0	
1806	V1-16	lambda	90	0	

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SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1807	V1-4	lambda	94	0	
1808	V1-4	lambda	94	0	
1809	V1-19	lambda	83	0	
1810	V1-4	lambda	93	0	
1811	V1-4	lambda	94	0	
1812	V1-16	lambda	90	0	
1813	V1-4	lambda	94	0	
1814	V1-4	lambda	94	0	
1815	V1-16	lambda	89	0	
1816	V2-13	lambda	91	-1	
1817	V2-13	lambda	90	-1	
1818	V2-13	lambda	98	-1	
1819	V1-4	lambda	94	0	
1820	V1-4	lambda	94	0	
1821	V1-4	lambda	94	0	
1822	V1-4	lambda	94	0	
1823	V2-13	lambda	90	-1	
1824	V1-4	lambda	93	0	
1825	V1-4	lambda	94	0	
1826	V2-13	lambda	98	-1	
1827	V1-4	lambda	93	0	
1828	V1-13	lambda	90	1	A
1829	V2-13	lambda	100	2	AL
1830	V2-14	lambda	91	1	A
1831	V1-13	lambda	91	1	A
1832	V1-16	lambda	95	1	A
1833	V2-13	lambda	89	2	AL
1834	V1-13	lambda	92	1	A
1835	V2-13	lambda	100	2	AL
1836	V1-13	lambda	92	1	A
1837	V1-19	lambda	93	1	A
1838	V3-2	lambda	81	1	A
1839	V1-13	lambda	94	1	A
1840	V1-19	lambda	91	1	A
1841	V1-13	lambda	92	1	A
1842	V2-1	lambda	89	1	A
1843	V1-20	lambda	81	2	AL
1844	L16	kappa	89	2	AL
1845	V1-16	lambda	93	2	AL
1846	V1-16	lambda	88	1	A
1847	V1-13	lambda	95	1	A
1848	V2-13	lambda	85	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1849	V1-18	lambda	84	1	A
1850	V1-16	lambda	81	1	A
1851	V1-16	lambda	90	2	AL
1852	V1-16	lambda	85	1	A
1853	V2-13	lambda	86	2	AL
1854	V1-2	lambda	83	1	A
1855	V1-17	lambda	86	1	A
1856	V2-13	lambda	96	2	AL
1857	V1-2	lambda	83	1	A
1858	V2-13	lambda	91	2	AL
1859	V1-19	lambda	94	1	A
1860	V1-16	lambda	88	1	A
1861	V1-13	lambda	79	1	A
1862	V1-13	lambda	89	1	A
1863	V2-13	lambda	88	2	AL
1864	V1-13	lambda	92	1	A
1865	V1-16	lambda	94	1	A
1866	V2-13	lambda	86	2	AL
1867	V2-13	lambda	89	2	AL
1868	V1-4	lambda	94	0	
1869	V1-4	lambda	94	0	
1870	V1-4	lambda	94	0	
1871	V2-13	lambda	90	-1	
1872	V1-4	lambda	94	0	
1873	V2-13	lambda	90	-1	
1874	V1-4	lambda	94	0	
1875	V1-4	lambda	94	0	
1876	O12	kappa	89	0	
1877	V2-13	lambda	89	-1	
1878	V1-4	lambda	94	0	
1879	O12	kappa	89	0	
1880	V1-4	lambda	93	0	
1881	L19	kappa	96	0	
1882	L12	kappa	88	0	
1883	L12	kappa	88	0	
1884	V1-4	lambda	90	1	S
1885	V1-13	lambda	90	1	A
1886	V1-4	lambda	94	0	
1887	L12	kappa	87	0	
1888	V1-4	lambda	90	0	
1889	L12	kappa	88	0	
1890	V1-16	lambda	95	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1891	V1-17	lambda	85	1	A
1892	V1-13	lambda	94	1	A
1893	V1-17	lambda	89	2	AL
1894	V1-17	lambda	85	1	A
1895	V1-13	lambda	90	1	A
1896	A27	kappa	90	2	AL
1897	V1-13	lambda	95	1	A
1898	V1-4	lambda	80	0	
1899	V1-19	lambda	83	0	
1900	L12	kappa	88	0	
1901	L12	kappa	88	0	
1902	L12	kappa	88	0	
1903	V2-14	lambda	91	2	AL
1904	V1-17	lambda	85	1	A
1905	V1-16	lambda	90	0	
1906	O12	kappa	89	0	
1907	V2-13	lambda	98	-1	
1908	V1-4	lambda	93	0	
1909	V1-4	lambda	82	0	
1910	V1-4	lambda	94	0	
1911	V2-13	lambda	97	-1	
1912	V2-13	lambda	98	-1	
1913	V1-19	lambda	83	0	
1914	V2-13	lambda	97	-1	
1915	L11	kappa	92	0	
1916	V1-4	lambda	82	0	
1917	V1-19	lambda	83	0	
1918	V1-4	lambda	93	0	
1919	V2-13	lambda	98	-1	
1920	L12	kappa	88	0	
1921	L11	kappa	92	0	
1922	L12	kappa	88	0	
1923	L18	kappa	85	0	
1924	V2-13	lambda	97	-1	
1925	V1-4	lambda	93	0	
1926	V1-19	lambda	83	0	
1927	V1-19	lambda	81	0	
1928	V1-19	lambda	82	0	
1929	V2-13	lambda	98	-1	
1930	V1-4	lambda	94	0	
1931	V2-13	lambda	97	-1	
1932	A20	kappa	89	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1933	V2-13	lambda	90	0	
1934	V1-19	lambda	83	0	
1935	L12	kappa	88	0	
1936	V1-19	lambda	83	0	
1937	V2-13	lambda	97	-1	
1938	V2-13	lambda	95	-1	
1939	V2-13	lambda	97	-1	
1940	V2-13	lambda	98	-1	
1941	V2-13	lambda	98	-1	
1942	V2-13	lambda	98	-1	
1943	L12	kappa	88	0	
1944	V2-13	lambda	97	-1	
1945	L12	kappa	88	0	
1946	V1-4	lambda	93	0	
1947	V2-13	lambda	97	-1	
1948	L12	kappa	88	0	
1949	V1-19	lambda	88	1	A
1950	V1-13	lambda	91	1	A
1951	V1-13	lambda	93	1	A
1952	L16	kappa	96	2	AL
1953	V1-13	lambda	93	1	A
1954	V1-16	lambda	79	1	A
1955	V2-13	lambda	95	2	AL
1956	V1-17	lambda	88	1	A
1957	V1-16	lambda	73	2	AL
1958	V1-16	lambda	92	1	A
1959	V2-13	lambda	91	2	AL
1960	V1-13	lambda	85	1	A
1961	V1-13	lambda	91	1	A
1962	V1-19	lambda	88	1	A
1963	V1-16	lambda	93	1	A
1964	A17	kappa	98	2	AL
1965	V2-17	lambda	77	2	AL
1966	V2-17	lambda	91	2	AL
1967	V1-13	lambda	90	1	A
1968	V1-13	lambda	95	1	A
1969	V1-13	lambda	91	1	A
1970	V1-13	lambda	90	1	A
1971	V1-17	lambda	87	1	A
1972	L19	kappa	88	2	AL
1973	V1-13	lambda	96	1	A
1974	V2-17	lambda	77	2	AL

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
1975	V2-13	lambda	100	2	AL
1976	V1-16	lambda	91	1	A
1977	V1-13	lambda	91	1	A
1978	V1-13	lambda	91	1	A
1979	V2-13	lambda	91	2	AL
1980	V2-13	lambda	87	2	AL
1981	V1-16	lambda	88	1	A
1982	V1-16	lambda	90	1	A
1983	V1-13	lambda	92	1	A
1984	V1-13	lambda	93	1	A
1985	V1-16	lambda	88	2	AL
1986	V1-17	lambda	88	1	A
1987	V1-17	lambda	87	1	A
1988	V2-13	lambda	95	2	AL
1989	V2-13	lambda	92	2	AL
1990	V2-13	lambda	92	2	AL
1991	A17	kappa	96	2	AL
1992	V2-17	lambda	97	2	AL
1993	V1-16	lambda	87	1	A
1994	V1-17	lambda	89	2	AL
1995	V2-1	lambda	93	1	A
1996	V1-16	lambda	89	1	A
1997	V1-13	lambda	92	1	A
1998	V1-16	lambda	87	1	A
1999	V1-13	lambda	93	1	A
2000	V1-16	lambda	91	1	A
2001	V1-13	lambda	90	2	AL
2002	V2-13	lambda	93	2	AL
2003	O12	kappa	89	0	
2004	V1-4	lambda	94	0	
2005	O12	kappa	89	0	
2006	V2-13	lambda	96	-1	
2007	V1-16	lambda	90	0	
2008	V2-13	lambda	97	-1	
2009	V1-4	lambda	93	0	
2010	V2-13	lambda	97	-1	
2011	V1-4	lambda	93	0	
2012	V1-4	lambda	94	0	
2013	V2-13	lambda	98	-1	
2014	V2-13	lambda	98	-1	
2015	V2-13	lambda	96	-1	
2016	V1-16	lambda	90	0	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
2017	O12	kappa	89	0	
2018	V2-13	lambda	98	-1	
2019	O12	kappa	89	0	
2020	O12	kappa	89	0	
2021	V2-13	lambda	97	-1	
2022	V2-13	lambda	97	-1	
2023	V2-13	lambda	97	-1	
2024	V2-13	lambda	96	0	
2025	V1-16	lambda	90	0	
2026	V1-4	lambda	94	0	
2027	O12	kappa	89	0	
2028	O12	kappa	89	0	
2029	V1-16	lambda	89	0	
2030	V1-16	lambda	89	0	
2031	V2-13	lambda	98	-1	
2032	V2-13	lambda	93	-1	
2033	V2-13	lambda	98	-1	
2034	V1-16	lambda	85	0	
2035	V2-13	lambda	97	-1	
2036	V2-13	lambda	95	-1	
2037	V1-4	lambda	94	0	
2038	V2-13	lambda	98	-1	
2039	V2-13	lambda	98	-1	
2040	O12	kappa	89	0	
2041	V1-16	lambda	87	0	
2042	V1-4	lambda	94	0	
2043	O12	kappa	89	0	
2044	V1-16	lambda	90	0	
2045	V1-16	lambda	89	0	
2046	V2-13	lambda	98	-1	
2047	V1-4	lambda	94	0	
2048	V1-16	lambda	90	0	
2049	V1-19	lambda	83	0	
2050	V1-4	lambda	94	0	
2051	V1-4	lambda	82	0	
2052	V1-4	lambda	94	0	
2053	O12	kappa	89	0	
2054	A20	kappa	90	0	
2055	V1-4	lambda	89	0	
2056	V2-13	lambda	98	-1	
2057	V2-13	lambda	91	-1	
2058	V2-13	lambda	98	-1	

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
2059	V1-4	lambda	94	0	
2060	V2-13	lambda	96	-1	
2061	V1-4	lambda	94	0	
2062	L12	kappa	88	0	
2063	L12	kappa	88	0	
2064	L12	kappa	88	0	
2065	V1-2	lambda	85	4	AASA
2066	V2-13	lambda	98	-1	
2067	V2-13	lambda	90	-1	
2068	V2-13	lambda	91	-1	
2069	V2-1	lambda	89	1	A
2070	V1-16	lambda	87	1	A
2071	V1-13	lambda	90	1	A
2072	V2-13	lambda	81	2	AL
2073	V1-13	lambda	89	1	A
2074	V1-13	lambda	90	1	A
2075	O12	kappa	88	2	AL
2076	V1-13	lambda	89	1	A
2077	V1-4	lambda	91	1	A
2078	V1-13	lambda	95	1	A
2079	V1-4	lambda	93	1	A
2080	V1-4	lambda	91	1	A
2081	A19	kappa	99	2	AL
2082	V1-13	lambda	92	1	A
2083	V1-16	lambda	94	1	A
2084	V2-13	lambda	93	2	AL
2085	V1-17	lambda	85	1	A
2086	V1-13	lambda	88	1	A
2087	V1-13	lambda	92	1	A
2088	V2-13	lambda	93	2	AL
2089	V1-4	lambda	95	1	A
2090	V1-4	lambda	85	1	A
2091	V1-17	lambda	95	1	A
2092	V1-13	lambda	98	1	A
2093	V1-13	lambda	90	1	A
2094	V1-13	lambda	89	1	A
2095	V1-13	lambda	89	1	A
2096	V1-17	lambda	90	2	AL
2097	V1-13	lambda	91	1	A
2098	V1-13	lambda	89	1	A
2099	V1-16	lambda	88	2	AL
2100	V1-13	lambda	91	1	A

Exhibit F

SEQ ID NO:X	VL germline sequence with highest percent identity to SEQ ID NO:X	Isotype of VL germline sequence with highest percent identity to SEQ ID NO:X	% Identity between VL germline sequence and SEQ ID NO:X	Number of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no 1 in VL region	Identity of amino acids after $(Gly_4Ser)_3$ sequence prior to amino acid position no. 1 in VL region
2101	V1-13	lambda	91	1	A
2102	V2-13	lambda	93	2	AL
2103	V2-13	lambda	93	2	AL
2104	O12	kappa	89	0	
2105	V1-16	lambda	90	0	
2106	V2-13	lambda	98	-1	
2107	V2-13	lambda	98	-1	
2108	V1-16	lambda	89	0	
2109	V1-4	lambda	94	0	
2110	O12	kappa	88	0	
2111	O12	kappa	88	0	
2112	V2-13	lambda	98	-1	
2113	V1-16	lambda	89	0	
2114	O12	kappa	89	0	
2115	O12	kappa	88	0	
2116	V1-4	lambda	94	0	
2117	V1-16	lambda	90	0	
2118	O12	kappa	89	0	
2119	V1-16	lambda	94	1	A
2120	V1-17	lambda	84	1	A
2121	V2-13	lambda	95	2	AL
2122	V1-17	lambda	85	1	A
2123	V1-16	lambda	89	1	A
2124	V1-13	lambda	86	1	A
2125	V1-16	lambda	91	1	A
2126	V1-13	lambda	89	1	A
2127	V1-13	lambda	89	1	A
2128	V1-16	lambda	89	1	A

SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

FIFTH EDITION

Tabulation and Analysis of
Amino Acid and Nucleic Acid Sequences of Precursors,
V-Regions, C-Regions, J-Chain, T-Cell Receptors for Antigen,
T-Cell Surface Antigens, β_2-Microglobulins,
Major Histocompatibility Antigens, Thy-1, Complement,
C-Reactive Protein, Thymopoietin, Integrins, Post-gamma Globulin,
α_2-Macroglobulins, and Other Related Proteins

1991

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TABLE I

Amino Acid Residues Associated with Framework (FR) and Complementarity Determining Regions (CDR) of the Variable Domains of Immunoglobulin Light (V_L) and Heavy (V_H) Chains

Segment	Light Chain	Heavy Chain
FR1	1-23 (with an occasional residue at 0, and a deletion at 10 in V_λ chains)	1-30 (with an occasional residue at 0)
CDR1	24-34 (with possible insertions numbered as 27A,B,C,D,E,F)	31-35 (with possible insertions numbered as 35A,B)
FR2[a]	35-49[a]	36-49
CDR2	50-56	50-65 (with possible insertions numbered as 52A,B,C)[b]
FR3	57-88	66-94 (with possible insertions numbered as 82A,B,C)
CDR3	89-97 (with possible insertions numbered as 95A,B,C,D,E,F)	95-102 (with possible insertions numbered as 100A,B,C,D,E,F,G,H,I,J,K)
FR4	98-107 (with a possible insertion numbered as 106A)	103-113

[a] Five Basilea rabbits (λ) immunized with type II pneumococci and which produced anti-type II pneumococcal polysaccharide had Met at position 48 and an insertion of four amino acid residues between positions 48 and 49; in four of the five the sequence was Glu, Leu, Lys, Ser and the fifth was Trp, Leu, Arg, Lys (53,54,63,64); the others were not sequenced at these positions (for references see table of rabbit λ amino acid sequences.)

[b] In the rabbit, Mage et al. (65) consider position 65 in V_H to be in FR3, since it is allotype related.

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Kabat Database and its applications: 30 years after the first variability plot

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ABSTRACT

The Kabat Database was initially started in 1970 to determine the combining site of antibodies based on the available amino acid sequences at that time. Bence Jones proteins, mostly from human, were aligned, using the now-known Kabat numbering system, and a quantitative measure, variability, was calculated for every position. Three peaks, at positions 24–34, 50–56 and 89–97, were identified and proposed to form the complementarity determining regions (CDR) of light chains. Subsequently, antibody heavy chain amino acid sequences were also aligned using a different numbering system, since the locations of their CDRs (31–35B, 50–65 and 95–102) are different from those of the light chains. CDRL1 starts right after the first invariant Cys 23 of light chains, while CDRH1 is eight amino acid residues away from the first invariant Cys 22 of heavy chains. During the past 30 years, the Kabat database has grown to include nucleotide sequences, sequences of T cell receptors for antigens (TCR), major histocompatibility complex (MHC) class I and II molecules and other proteins of immunological interest. It has been used extensively by immunologists to derive useful structural and functional information from the primary sequences of these proteins. An overall view of the Kabat Database and its various applications are summarized here. The Kabat Database is freely available at http://immuno.bme.nwu.edu

INTRODUCTION

The purpose of maintaining the Kabat Database of aligned sequences of proteins of immunological interest, in our opinion, is to provide useful correlations between structure and function for this special group of proteins from their nucleotide and amino acid sequences to their tertiary structures (1). These sequences are thus aligned with the ultimate aim of understanding how these proteins are folded and how they can perform their biological functions. We include only coding region sequences that have been published. In some cases, only the amino acid sequences were published, while the corresponding nucleotide sequences were deposited in GenBank. All stored sequences were then printed out and checked visually against available published sequences. We routinely survey for possible new sequences in journals in our libraries, Medline entries, cross-references from other papers, and author notification; however, we may still miss some sequences. GenBank, on the other hand, contains a substantial number of unpublished sequences. If there are doubts about these sequences or their annotations, please refer to the original papers. The Kabat numbering systems (see the Introduction of 2) for antibody light and heavy chains, for TCR alpha and beta chains, etc., go hand-in-hand with variability calculations. The locations of the CDRs are the theoretically derived positions which can be verified experimentally. Indeed, from the first antigen–antibody Fab complex (3) to the complexes of TCR, processed peptide and MHC class I molecule (4,5), it has been realized that alignment of amino acid sequences and variability calculations can be of utmost importance in understanding how these important macromolecules function biologically. Due to the rapid development of genetic and protein engineering methods, mouse and rat antibodies have been humanized to treat human cancers, viral infections, etc (6). CDRs of selected rodent antibodies are cut out and glued onto human antibody frameworks to minimize rejection by human patients.

Our predicted CDRs are slightly different from Chothia's. A careful comparison can be found from a hyperlink on our website to 'Andrew's Antibody Page' (http://www.biochem.ucl.ac.uk/~martin/abs/index.html).

Massive amounts of sequence data are being continuously published in the scientific literature. It is imperative to collect and properly align the sequences so that they can be used by as many researchers in this field as possible. We have previously published five editions of these sequences (see the Introduction of 2). In 1991, the fifth edition (2) consisted of three volumes. Currently, the database is more than five times as large. As of September 29, 1999, the Kabat database contained 1 599 375 and 2 517 756 nt for antibody light and heavy chain variable regions, respectively, as compared to 272 244 and 418 962 nt in 1991. Total numbers of entries, amino acids and bases of other categories of sequences can be obtained by using the 'Current Counts' hyperlink on our website. The collection is available on our website (http://www.immuno.bme.nwu.edu) which is free due to the generous support by various research grants from NIH since 1970.

Finally, numerous scientific papers have cited our database, quoting our fourth edition (7), fifth edition (2), or one of our more recent papers (8). On our part, we have been analyzing

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the Kabat Database during the past few years with reference to the total numbers of antibody and TCR V-genes, possible evolutionary selection processes, importance of antibody CDRH3s as related to their fine specificities, etc.

KABAT DATABASE

The Kabat Database may be accessed for searching, sequence retrieval and analysis by a few different methods: electronic mail, WWW and ftp. The electronic mail interface has been available since 1993, the WWW interface since 1995 and various formats of the database in electronic format for nearly a decade (8). Our data formats, searching tools, output formats and database structures have gradually been adopted by other immunological databases and interfaces.

Electronic mail interface

An electronic mail interface (seqhunt2@immuno.bme.nwu.edu) provides a non-interactive method for searching and sequence retrieval (9). Sending mail to the server address with the single word 'help' (no quotes) in the message body returns instructions for using the server.

All sequences classes are searchable and returnable. The query format allows making AND/OR/NOT constructed restrictions on the database and amino acid and nucleotide sequence pattern matching with allowable differences. Requests are processed as they are received and depending on the network traffic, take ~1–2 min to be searched and returned to the sender. The returned format is a fixed-line length record of 80 or fewer characters per line for ease in visual inspection and processing by user-written scripts or programs. The characters are plain text.

The query format for the sent request consists of two parts. The first part contains directives for the server to follow while the second part contains specifications of the search. Specification of the extent of data returned, the number of documents to return, starting document and whether plain ASCII text or PostScript should be used in the return format may be entered. Further, one can direct the server to return a distribution, the variability or unaligned raw data for the search specified.

The second part of the query contains the search restrictions on the database. Words separated by AND and OR may be used, as well as searching functions, like nucleotide/amino acid pattern matching and positional restriction matching.

There are basically three steps in translating and performing a search on the Kabat Database: generate the question or query, translate it into a format the server can recognize and decide on the output options desired of the returned matches. For example, if matches of mouse kappa light chains of anti-phosphorylcholine antibodies are desired, the query and restriction on the database would be:

Begin
@mouse and kappa and phosphorylcholine

The '@' before mouse tells the server that matches of the species mouse are desired, rather than searching through the entire database record for instances of the word 'mouse'. More complicated restrictions can be generated using parentheses for grouping and the minus sign '–' for NOT. Finding all rat and rabbit sequences which are not kappa light chains, and returning them as amino acid sequences in PostScript format would be constructed as:

PSAA
Begin
(rat and rabbit) and –kappa

Pattern matching is interpreted as the second part of an AND statement, such that finding all rat and rabbit sequences which are not kappa and contain the nucleotide pattern cagtacgtcag with three allowable mismatches, would be sent as:

Begin
(rat and rabbit) and –kappa [implicit AND]
#NM 3
cagtacgtcag

More examples of searching and output options may be found in the 'help' file returned from the server.

WWW interface

The WWW interface (8) to the Kabat Database: http://immuno.bme.nwu.edu contains searching and analysis tools as well as links to database download sites and other interesting databases. Most of the features found in the electronic mail interface are found in the WWW interface, as well as other tools. The WWW interface is more interactive than the Email and returns results faster, depending on the network traffic.

Searching and analysis tools

SeqhuntII. This grouping of programs allows searches through the annotations and sequence pattern matching of the amino acid and nucleotide sequence data with allowable mismatches. Like the Email server, restrictions on the database may be formulated as AND/OR/NOT constructs. Output extent, output format, maximum documents and starting document may be specified. Browsing of the output results in HTML format allows the user to view the database entries in an easy-to-read format. ASCII text may be selected as output for use in user-generated scripts and programs. PostScript generation allows for printing on a PostScript supporting printer. Sequence matching is returned aligned with the target sequence with nucleotide or amino acid differences from the database sequence displayed in a case change. Since the database contains only coding regions of genes and proteins, the query sequence should be a portion of the coding region being sought.

Variability. Variability and amino acid distributions of sequence groups may be generated for restrictions on the database. The variability plots are in PostScript format and may either be viewed on the screen with an appropriate PostScript viewer (e.g. GNU ghostscript or ghostview) or printed to a postscript-supporting printer. Plots for human and mouse TCR gamma and delta chain variable regions are shown in Figure 1. Scaling of the variability plots may be done allowing comparison of variability plots for different groupings of sequences. Distributions of the amino acids per position may be returned also, including the calculated variability for each position.

Sequence alignment. Alignment of user-entered coding regions of immunoglobulin light chains according to the Kabat numbering system can be performed. Because of the relatively few alignment options available for light chains, most sequences can be aligned. One can start with around 10 amino acid residues or 30 nt. There is no lower limit on the length of sequence to be matched. In some cases though, visual inspection and alignment is necessary, as is for heavy chain alignment,

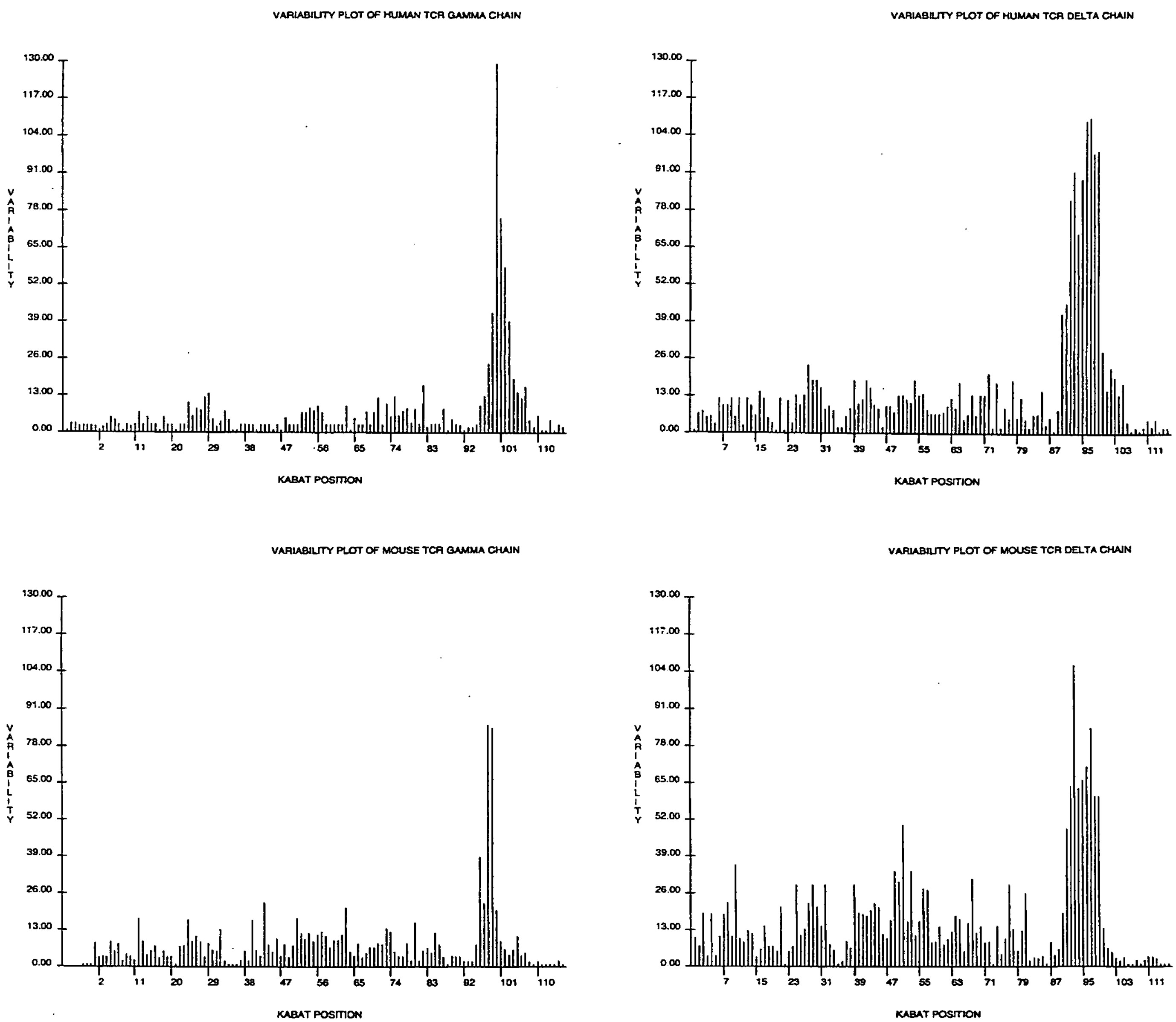

Figure 1. Variability plots for human and mouse TCR gamma and delta chain variable regions, using 377 human gamma, 1260 human delta, 297 mouse gamma and 461 mouse delta partial and complete sequences.

especially within the CDRH3 region, if additional codons or residues are inserted and denoted by '#'. If a suitable alignment counterpart from the database is not found for the target sequence, the user can contact us.

FTP. Various formats of the database are available for download from NCBI's repository under the directory 'kabat'. Currently active formats include a FASTA-like raw sequence format and the database's fixed length format of 80 or fewer characters per line and vertical alignment. Four main variations on the fixed length format exist to properly visually display single translations, pseudogene translations, J-minigenes and D-minigenes. Other immunological databases have adopted similar formats as exemplified by the three letter code amino acid translation followed by single letter code. A 'dump' version of the database is periodically updated which contains unlimited line length records more suitable for mass processing on unix-based systems.

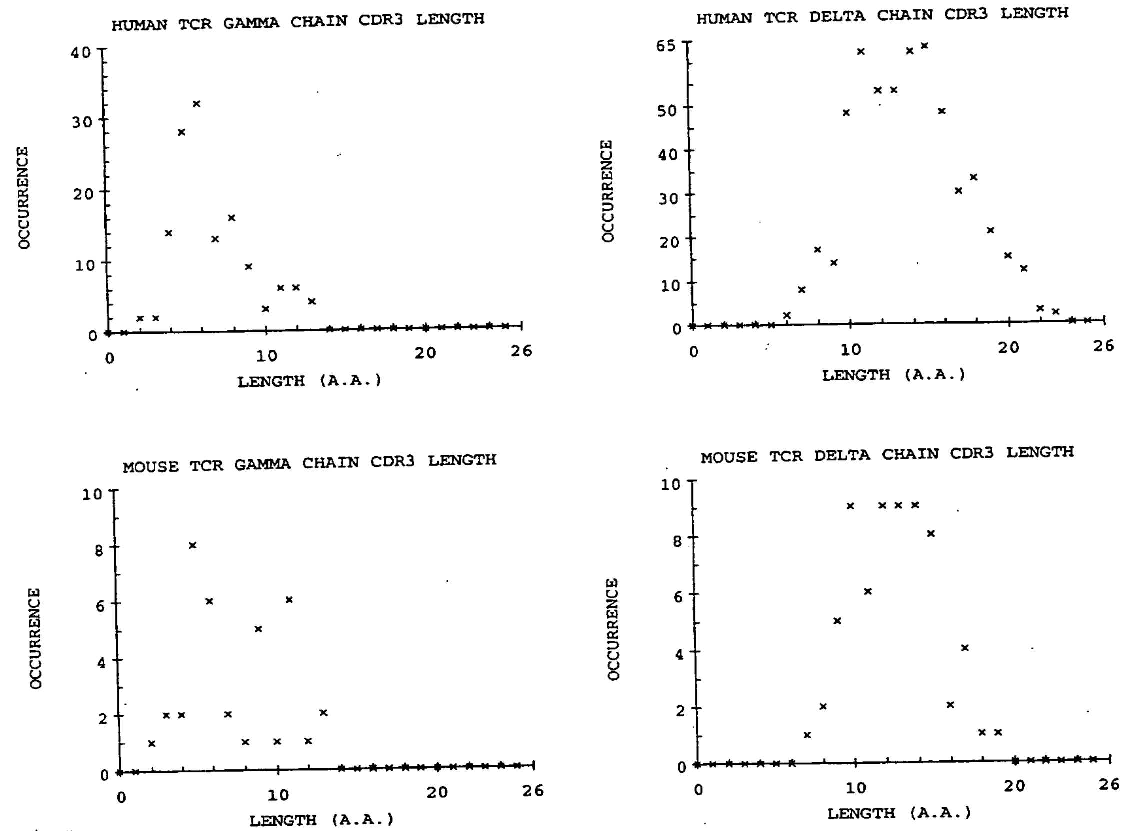

Figure 2. Length distributions of CDR3s of human and mouse TCR gamma and delta chains, based on 135 human gamma, 546 human delta, 37 mouse gamma and 66 mouse delta complete CDR3 sequences.

OTHER APPLICATIONS

As mentioned before, the Kabat Database was initially constructed for the purpose of identifying the antibody combining site (1). Starting from aligned amino acid sequences and using variability calculations, we have identified CDRs of antibody light and heavy chains, as well as those of TCRs. Such calculations can also provide useful predictions for MHC class I and II sequences (8), and to other aligned proteins sequences, e.g. HIV gp120, gp41, etc.

The importance of CDRH3 to confer fine specificity to antibodies was realized a few years ago (10). Furthermore, the unique CDRH3 nucleotide sequences have recently been used as a sensitive diagnostic test to detect residue B cell malignancies in cancer patients. Thus, many of these sequences have been determined. But most of them have been excluded from GenBank due to their relative short lengths. We have been meticulously collecting them, and realized the importance of their length distributions in antibodies of various specificities (11), and possible differences between CDRH3s of human and mouse (12). In the case of rabbit, the CDRH3s have less length variation than human and mouse. This may be compensated by the length variations of the CDRL3s (13).

The length variations of TCR alpha and beta chain CDR3s are very restricted (14). On the other hand, TCR gamma and delta chain CDR3s have more length variation, close to those of antibody heavy chains (Fig. 2). Whether they bind antigens directly is unclear.

During recent years, various research groups have decided to sequence the entire coding region of different antibody and TCR V-genes, in order to have an idea of their total numbers. On the other hand, we have discovered that pair-wise comparisons of V-gene nucleotide sequences in the Kabat Database provide very accurate estimations of their total numbers (15,16). In addition, such comparisons seem to suggest that antibody and TCR V-genes have evolved under different selective pressures (17). In the case of MHC class I sequences, comparison of their aligned sequences has elucidated a new mechanism of generating novel MHC class I molecules by random assortment of their a1 and a2 gene segments (18).

DISCUSSION

The Kabat Database has been around for 30 years. It has provided the immunology community a useful service, since it

not only is a sequence database but also incorporates vital aspects of the biology of the immune system. Various analytical methods have been developed to study the structure and function relations of proteins of immunological interest.
Electronic addresses:
http://immuno.bme.nwu.edu
seqhunt2@immuno.bme.nwu.edu
Citing the Kabat Database:
Authors using this database may cite this paper together with the electronic addresses.

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